



SEQUENCE LISTING

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<110> SHIMKETS, RICHARD A
FERNANDES, ELMA

<120> POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY

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<140> 09/635,949

<141> 2000-08-10

<150> USSN 60/148,433

<151> 1999-08-11

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<170> PatentIn Ver. 2.1

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<211> 1867

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<213> Homo sapiens

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Tyr Met Cys Gln Tyr Asp Tyr Val Glu Val Arg Asp Gly Asp Asn Arg
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 485 490 495
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 Gln Leu Leu Leu Ile Ser Ser Leu Pro Arg Glu Tyr Thr Val Ile Asn
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Gly Tyr Thr Ile Pro Cys Cys Arg Asn Glu Glu Asn Glu Cys Asp Ser
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Cys Leu Ile His Pro Gly Cys Thr Ile Phe Glu Asn Cys Lys Ser Cys
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Arg Cys Gly Gln Val Leu Arg Ala Pro Lys Gly Gln Ile Leu Leu Glu
130 135 140

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Ser Tyr Pro Leu Asn Ala His Cys Glu Trp Thr Ile His Ala Lys Pro
145 150 155

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Asp Gly Gln Ile Ile Lys Arg Val Cys Gly Asn Glu Arg Pro Ala Pro
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Ile Ser Pro Phe Tyr Arg Arg Leu Gly Ser Ser Arg Lys Thr Cys Leu
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 Gly Leu Val Ser Trp Ser Tyr Asp Lys Thr Cys Ser His Arg Leu Ser
 690 695 700

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Ser Pro Gly Phe Lys Asn Asp Thr Leu Arg Ser Gly Val Val Ser Val		
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Ser Ile Phe Leu Ile Gly Thr Lys Ile Gly Leu Phe Leu Gln Val Ala
10 15 20
cct cta tca gtt atg gct aaa tcc tgt cca tct gtg tgt cgc tgc gat 571
Pro Leu Ser Val Met Ala Lys Ser Cys Pro Ser Val Cys Arg Cys Asp
25 30 35
gcg ggt ttc att tac tgt aat gat cgc ttt ctg aca tcc att cca aca 619
Ala Gly Phe Ile Tyr Cys Asn Asp Arg Phe Leu Thr Ser Ile Pro Thr
40 45 50
gga ata cca gag gat gct aca act ctc tac ctt cag aac aac caa ata 667
Gly Ile Pro Glu Asp Ala Thr Thr Leu Tyr Leu Gln Asn Asn Gln Ile
55 60 65 70
aat aat gct ggg att cct tca gat ttg aaa aac ttg ctg aaa gta gaa 715
Asn Asn Ala Gly Ile Pro Ser Asp Leu Lys Asn Leu Leu Lys Val Glu
75 80 85
aga ata tac cta tac cac aac agt tta gat gaa ttt cct acc aac ctc 763
Arg Ile Tyr Leu Tyr His Asn Ser Leu Asp Glu Phe Pro Thr Asn Leu
90 95 100

cca aag tat gta aaa gag tta cat ttg caa gaa aat aac ata agg act 811
 Pro Lys Tyr Val Lys Glu Leu His Leu Gln Glu Asn Asn Ile Arg Thr
 105 110 115

atc act tat gat tca ctt tca aaa att ccc tat ctg gaa gaa tta cat 859
 Ile Thr Tyr Asp Ser Leu Ser Lys Ile Pro Tyr Leu Glu Glu Leu His
 120 125 130

tta gat gac aac tct gtc tct gca gtt agc ata gaa gag gga gca ttc 907
 Leu Asp Asp Asn Ser Val Ser Ala Val Ser Ile Glu Glu Gly Ala Phe
 135 140 145 150

cga gac agc aac tat ctc cga ctg ctt ttc ctg tcc cgt aat cac ctt 955
 Arg Asp Ser Asn Tyr Leu Arg Leu Leu Phe Leu Ser Arg Asn His Leu
 155 160 165

agc aca att ccc tgg ggt ttg ccc agg act ata gaa gaa cta cgc ttg 1003
 Ser Thr Ile Pro Trp Gly Leu Pro Arg Thr Ile Glu Glu Leu Arg Leu
 170 175 180

gat gat aat cgc ata tcc act att tca tca cca tct ctt caa ggt ctc 1051
 Asp Asp Asn Arg Ile Ser Thr Ile Ser Ser Pro Ser Leu Gln Gly Leu
 185 190 195

act agt cta aaa cgc ctg gtt cta gat gga aac ctg ttg aac aat cat 1099
 Thr Ser Leu Lys Arg Leu Val Leu Asp Gly Asn Leu Leu Asn Asn His
 200 205 210

ggt tta ggt gac aaa gtt ttc ttc aac cta gtt aat ttg aca gag ctg 1147
 Gly Leu Gly Asp Lys Val Phe Phe Asn Leu Val Asn Leu Thr Glu Leu
 215 220 225 230

tcc ctg gtg cgg aat tcc ctg act gct gca cca gta aac ctt cca ggc 1195
 Ser Leu Val Arg Asn Ser Leu Thr Ala Ala Pro Val Asn Leu Pro Gly
 235 240 245

aca aac ctg agg aag ctt tat ctt caa gat aac cac atc aat cgg gtg 1243
 Thr Asn Leu Arg Lys Leu Tyr Leu Gln Asp Asn His Ile Asn Arg Val
 250 255 260

ccc cca aat gct ttt tct tat cta agg cag ctc tat cga ctg gat atg 1291
 Pro Pro Asn Ala Phe Ser Tyr Leu Arg Gln Leu Tyr Arg Leu Asp Met
 265 270 275

tcc aat aat aac cta agt aat tta cct cag ggt atc ttt gat gat ttg 1339
 Ser Asn Asn Asn Leu Ser Asn Leu Pro Gln Gly Ile Phe Asp Asp Leu
 280 285 290

gac aat ata aca caa ctg att ctt cgc aac aat ccc tgg tat tgc ggg 1387
 Asp Asn Ile Thr Gln Leu Ile Leu Arg Asn Asn Pro Trp Tyr Cys Gly
 295 300 305 310

tgc aag atg aaa tgg gta cgt gac tgg tta caa tca cta cct gtg aag 1435
Cys Lys Met Lys Trp Val Arg Asp Trp Leu Gln Ser Leu Pro Val Lys
315 320 325

gtc aac gtg cgt ggg ctc atg tgc caa gcc cca gaa aag gtt cgt ggg 1483
Val Asn Val Arg Gly Leu Met Cys Gln Ala Pro Glu Lys Val Arg Gly
330 335 340

atg gct att aag gat ctc aat gca gaa ctg ttt gat tgt aag gac agt 1531
Met Ala Ile Lys Asp Leu Asn Ala Glu Leu Phe Asp Cys Lys Asp Ser
345 350 355

ggg att gta agc acc att cag ata acc act gca ata ccc aac aca gtg 1579
Gly Ile Val Ser Thr Ile Gln Ile Thr Thr Ala Ile Pro Asn Thr Val
360 365 370

tat cct gcc caa gga cag tgg cca gct cca gtg acc aaa cag cca gat 1627
Tyr Pro Ala Gln Gly Gln Trp Pro Ala Pro Val Thr Lys Gln Pro Asp
375 380 385 390

att aag aac ccc aag ctc act aag gat caa caa acc aca ggg agt ccc 1675
Ile Lys Asn Pro Lys Leu Thr Lys Asp Gln Gln Thr Thr Gly Ser Pro
395 400 405

tca aga aaa aca att aca att act gtg aag tct gtc acc tct gat acc 1723
Ser Arg Lys Thr Ile Thr Ile Thr Val Lys Ser Val Thr Ser Asp Thr
410 415 420

att cat atc tct tgg aaa ctt gct cta cct atg act gct ttg aga ctc 1771
Ile His Ile Ser Trp Lys Leu Ala Leu Pro Met Thr Ala Leu Arg Leu
425 430 435

agc tgg ctt aaa ctg ggc cat agc ccg gca ttt gga tct ata aca gaa 1819
Ser Trp Leu Lys Leu Gly His Ser Pro Ala Phe Gly Ser Ile Thr Glu
440 445 450

aca att gta aca ggg gaa cgc agt gag tac ttg gtc aca gcc ctg gag 1867
Thr Ile Val Thr Gly Glu Arg Ser Glu Tyr Leu Val Thr Ala Leu Glu
455 460 465 470

cct gat tca ccc tat aaa gta tgc atg gtt ccc atg gaa acc agc aac 1915
Pro Asp Ser Pro Tyr Lys Val Cys Met Val Pro Met Glu Thr Ser Asn
475 480 485

ctc tac cta ttt gat gaa act cct gtt tgt att gag act gaa act gca 1963
Leu Tyr Leu Phe Asp Glu Thr Pro Val Cys Ile Glu Thr Glu Thr Ala
490 495 500

ccc ctt cga atg tac aac cct aca acc acc ctc aat cga gag caa gag 2011
Pro Leu Arg Met Tyr Asn Pro Thr Thr Thr Leu Asn Arg Glu Gln Glu
505 510 515

aaa gaa cct tac aaa aac ccc aat tta cct ttg gct gcc atc att ggt 2059

Lys Glu Pro Tyr Lys Asn Pro Asn Leu Pro Leu Ala Ala Ile Ile Gly
520 525 530

ggg gct gtg gcc ctg gtt acc att gcc ctt ctt gct tta gtg tgt tgg 2107
Gly Ala Val Ala Leu Val Thr Ile Ala Leu Leu Ala Leu Val Cys Trp
535 540 545 550

tat gtt cat agg aat gga tcg ctc ttc tca agg aac tgt gca tat agc 2155
Tyr Val His Arg Asn Gly Ser Leu Phe Ser Arg Asn Cys Ala Tyr Ser
555 560 565

aaa ggg agg aga aga aag gat gac tat gca gaa gct ggc act aag aag 2203
Lys Gly Arg Arg Lys Asp Asp Tyr Ala Glu Ala Gly Thr Lys Lys
570 575 580

gac aac tct atc ctg gaa atc agg gaa act tct ttt cag atg tta cca 2251
Asp Asn Ser Ile Leu Glu Ile Arg Glu Thr Ser Phe Gln Met Leu Pro
585 590 595

ata agc aat gaa ccc atc tcg aag gag gag ttt gta ata cac acc ata 2299
Ile Ser Asn Glu Pro Ile Ser Lys Glu Glu Phe Val Ile His Thr Ile
600 605 610

ttt cct cct aat gga atg aat ctg tac aaa aac aat cac agt gaa agc 2347
Phe Pro Pro Asn Gly Met Asn Leu Tyr Lys Asn Asn His Ser Glu Ser
615 620 625 630

agt agt aac cga agc tac aga gac agt ggt att cca gac tca gat cac 2395
Ser Ser Asn Arg Ser Tyr Arg Asp Ser Gly Ile Pro Asp Ser Asp His
635 640 645

tca cac tca tgatgctgaa ggactcacag cagacttgtg ttttgggttt 2444
Ser His Ser

tttaaacta agggaggtga tggtaggaac cctgttctac tgcaaaacac tggaaaaaga 2504

gactgaaaaa aagcaatgta ctgtacatt gccatataat ttatatataa gaactttta 2564

ttaaaagttt caaatccag gttactgctg cgattgatgt agtggagatg cctgaacaca 2624

attctatatt ttagtatttt ttagtaattt gtactgtatt ttcttgcaa atattggagt 2684

tataaacat ttactttgtg ttctactgag taagatgact tgttgactgt gaaagtgaat 2744

tttctgctg tgtcgaacaa tcaggactgc attcatatga gatccttgta gtataagcac 2804

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<211> 649

<212> PRT

<213> Homo sapiens

<400> 6

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Leu Phe Leu Gln Val Ala Pro Leu Ser Val Met Ala Lys Ser Cys Pro
20 25 30

Ser Val Cys Arg Cys Asp Ala Gly Phe Ile Tyr Cys Asn Asp Arg Phe
35 40 45

Leu Thr Ser Ile Pro Thr Gly Ile Pro Glu Asp Ala Thr Thr Leu Tyr
50 55 60

Leu Gln Asn Asn Gln Ile Asn Asn Ala Gly Ile Pro Ser Asp Leu Lys
65 70 75 80

Asn Leu Leu Lys Val Glu Arg Ile Tyr Leu Tyr His Asn Ser Leu Asp
85 90 95

Glu Phe Pro Thr Asn Leu Pro Lys Tyr Val Lys Glu Leu His Leu Gln
100 105 110

Glu Asn Asn Ile Arg Thr Ile Thr Tyr Asp Ser Leu Ser Lys Ile Pro
115 120 125

Tyr Leu Glu Glu Leu His Leu Asp Asp Asn Ser Val Ser Ala Val Ser
130 135 140

Ile Glu Glu Gly Ala Phe Arg Asp Ser Asn Tyr Leu Arg Leu Leu Phe
145 150 155 160

Leu Ser Arg Asn His Leu Ser Thr Ile Pro Trp Gly Leu Pro Arg Thr
165 170 175

Ile Glu Glu Leu Arg Leu Asp Asp Asn Arg Ile Ser Thr Ile Ser Ser
180 185 190

Pro Ser Leu Gln Gly Leu Thr Ser Leu Lys Arg Leu Val Leu Asp Gly
195 200 205

Asn Leu Leu Asn Asn His Gly Leu Gly Asp Lys Val Phe Phe Asn Leu
210 215 220

Val Asn Leu Thr Glu Leu Ser Leu Val Arg Asn Ser Leu Thr Ala Ala
225 230 235 240

Pro Val Asn Leu Pro Gly Thr Asn Leu Arg Lys Leu Tyr Leu Gln Asp
245 250 255

Asn His Ile Asn Arg Val Pro Pro Asn Ala Phe Ser Tyr Leu Arg Gln
260 265 270

Leu Tyr Arg Leu Asp Met Ser Asn Asn Asn Leu Ser Asn Leu Pro Gln
275 280 285

Gly Ile Phe Asp Asp Leu Asp Asn Ile Thr Gln Leu Ile Leu Arg Asn
290 295 300

Asn Pro Trp Tyr Cys Gly Cys Lys Met Lys Trp Val Arg Asp Trp Leu
305 310 315 320

Gln Ser Leu Pro Val Lys Val Asn Val Arg Gly Leu Met Cys Gln Ala
325 330 335

Pro Glu Lys Val Arg Gly Met Ala Ile Lys Asp Leu Asn Ala Glu Leu
340 345 350

Phe Asp Cys Lys Asp Ser Gly Ile Val Ser Thr Ile Gln Ile Thr Thr
355 360 365

Ala Ile Pro Asn Thr Val Tyr Pro Ala Gln Gly Gln Trp Pro Ala Pro
370 375 380

Val Thr Lys Gln Pro Asp Ile Lys Asn Pro Lys Leu Thr Lys Asp Gln
385 390 395 400

Gln Thr Thr Gly Ser Pro Ser Arg Lys Thr Ile Thr Ile Thr Val Lys
405 410 415

Ser Val Thr Ser Asp Thr Ile His Ile Ser Trp Lys Leu Ala Leu Pro
420 425 430

Met Thr Ala Leu Arg Leu Ser Trp Leu Lys Leu Gly His Ser Pro Ala
435 440 445

Phe Gly Ser Ile Thr Glu Thr Ile Val Thr Gly Glu Arg Ser Glu Tyr
450 455 460

Leu Val Thr Ala Leu Glu Pro Asp Ser Pro Tyr Lys Val Cys Met Val
465 470 475 480

Pro Met Glu Thr Ser Asn Leu Tyr Leu Phe Asp Glu Thr Pro Val Cys
485 490 495

Ile Glu Thr Glu Thr Ala Pro Leu Arg Met Tyr Asn Pro Thr Thr Thr
500 505 510

Leu Asn Arg Glu Gln Glu Lys Glu Pro Tyr Lys Asn Pro Asn Leu Pro
515 520 525

Leu Ala Ala Ile Ile Gly Gly Ala Val Ala Leu Val Thr Ile Ala Leu
530 535 540

Leu Ala Leu Val Cys Trp Tyr Val His Arg Asn Gly Ser Leu Phe Ser
545 550 555 560

Arg Asn Cys Ala Tyr Ser Lys Gly Arg Arg Arg Lys Asp Asp Tyr Ala
565 570 575

Glu Ala Gly Thr Lys Lys Asp Asn Ser Ile Leu Glu Ile Arg Glu Thr
580 585 590

Ser Phe Gln Met Leu Pro Ile Ser Asn Glu Pro Ile Ser Lys Glu Glu
595 600 605

Phe Val Ile His Thr Ile Phe Pro Pro Asn Gly Met Asn Leu Tyr Lys
610 615 620

Asn Asn His Ser Glu Ser Ser Ser Asn Arg Ser Tyr Arg Asp Ser Gly
625 630 635 640

Ile Pro Asp Ser Asp His Ser His Ser
645

<210> 7

<211> 1653

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (964)..(1443)

<400> 7

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acttttttta tttctttttt tccatctctg ggccagcttg ggatcctagg ccgccctggg 120

aagacatttg tgttttacac acataaggat ctgtgtttgg ggtttcttct tcctcccctg 180

acattggcat tgcttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgctt 240

gcacttatct gcctaggtac atcgaagtct ttgacctcc atacagtgat tatgcctgtc 300

atcgctgggtg gtatcctggc ggccttgctc ctgctgatag ttgtcgtgct ctgtctttac 360

ttcaaaatac acaacgcgct aaaagctgca aaggaacctg aagctgtggc tgtaaaaaat 420

cacaaccag acaagggtg gtgggccaag aacagccagg ccaaaaccat tgccacggag 480

tctgtcctg cctgcagtg ctgtgaagga tatagaatgt gtgccagttt tgattccctg 540

ccaccttgct gttgcgacat aaatgagggc ctctgagtta ggaaaggctc ctttctcaaa 600

gcagagccct gaagacttca atgatgtcaa tgaggccacc tgtttgatgt gtgcaggcac 660

agaagaaagg cacagctccc catcagtttc atggaaaata actcagtgcc tgctgggaac 720
 cagctgctgg agatccctac agagagcttc cactgggggc aaccctcca ggaaggagtt 780
 ggggagagag aaccctcact gtggggaatg ctgataaacc agtcacacag ctgctctatt 840
 ctcacacaaa tctaccctt gcgtggctgg aactgacgtt tccctggagg tgtccagaaa 900
 gctgatgtaa cacagagcct ataaaagctg tcggtccta aggctgccca gcgccttgcc 960

 aaa atg gag ctt gta aga agg ctc atg cca ttg acc ctc tta att ctc 1008
 Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Ile Leu
 1 5 10 15

 tcc tgt ttg gcg gag ctg aca atg gcg gag gct gaa ggc aat gca agc 1056
 Ser Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser
 20 25 30

 tgc aca gtc agt cta ggg ggt gcc aat atg gca gag acc cac aaa gcc 1104
 Cys Thr Val Ser Leu Gly Ala Asn Met Ala Glu Thr His Lys Ala
 35 40 45

 atg atc ctg caa ctc aat ccc agt gag aac tgc acc tgg aca ata gaa 1152
 Met Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu
 50 55 60

 aga cca gaa aac aaa agc atc aga att atc ttt tcc tat gtc cag ctt 1200
 Arg Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu
 65 70 75

 gat cca gat gga agc tgt gaa agt gaa aac att aaa gtc ttt gac gga 1248
 Asp Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly
 80 85 90 95

 acc tcc agc aat ggg cct ctg cta ggg caa gtc tgc agt aaa aac gac 1296
 Thr Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp
 100 105 110

 tat gtt cct gta ttt gaa tca tca tcc agt aca ttg acg ttt caa ata 1344
 Tyr Val Pro Val Phe Glu Ser Ser Ser Ser Thr Leu Thr Phe Gln Ile
 115 120 125

 gtt act gac tca gca aga att caa aga act gtc ttt gtc ttc tac tac 1392
 Val Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr
 130 135 140

 ttc ttc tct cct aac atc tgg ctc tgc att cac agc acc tac att cca 1440
 Phe Phe Ser Pro Asn Ile Trp Leu Cys Ile His Ser Thr Tyr Ile Pro
 145 150 155

 ctg tgatccgaag cagaatgccagaagaatctg cgagtgggtt catgaggaga 1493
 Leu
 160

gctccactgt ggatttcttt ccaaggccca gagctgacca tgtcactctc ctgctaaaac 1553

cactgacttc ttggtaccag cagatctcca gagtgcagca gtcaagggtt tcccacgctg 1613

gaccagggcc ctgtcccatc aaaaaaaaaa aaaaaaaaaa 1653

<210> 8

<211> 160

<212> PRT

<213> Homo sapiens

<400> 8

Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser

1 5 10 15

Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys

20 25 30

Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met

35 40 45

Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg

50 55 60

Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp

65 70 75 80

Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr

85 90 95

Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr

100 105 110

Val Pro Val Phe Glu Ser Ser Ser Ser Thr Leu Thr Phe Gln Ile Val

115 120 125

Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe

130 135 140

Phe Ser Pro Asn Ile Trp Leu Cys Ile His Ser Thr Tyr Ile Pro Leu

145 150 155 160

<210> 9

<211> 2478

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (273)..(2012)

<400> 9

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aggtgtctc tcttgagaag aactgtccat accatggtagg tggtaggct ttcaccagtt 180

ctcaggatgc ccatagggat ggggaagcc tgctggcct gtggtgctt ccagtggccg 240

tcattctatt agggccccac agtggcatta gg atg cac ctc tcg gcg gtg ttc 293

Met His Leu Ser Ala Val Phe

1

5

aac gcc ctc ctg gtg tcg gtg ctg gca gcg gtc ctg tgg aag cat gtg 341

Asn Ala Leu Leu Val Ser Val Leu Ala Ala Val Leu Trp Lys His Val

10

15

20

cgg ctg cgt gag cat gca gcc aca ctg gag gag gag ctg gcc ctc agc 389

Arg Leu Arg Glu His Ala Ala Thr Leu Glu Glu Glu Leu Ala Leu Ser

25

30

35

cga cag gcc aca gag cca gcc cca gca ctg agg atc gac tac ccg aag 437

Arg Gln Ala Thr Glu Pro Ala Pro Ala Leu Arg Ile Asp Tyr Pro Lys

40

45

50

55

gca ctg cag atc ctg atg gag ggc ggc aca cac atg gtg tgc acg ggc 485

Ala Leu Gln Ile Leu Met Glu Gly Gly Thr His Met Val Cys Thr Gly

60

65

70

cgc acg cac aca gac cgc atc tgc cgc ttc aag tgg ctc tgc tac tcc 533

Arg Thr His Thr Asp Arg Ile Cys Arg Phe Lys Trp Leu Cys Tyr Ser

75

80

85

aac gag gct gag gag ttc atc ttc ttc cat ggc aac acc tct gtc atg 581

Asn Glu Ala Glu Glu Phe Ile Phe Phe His Gly Asn Thr Ser Val Met

90

95

100

ctg ccc aac ctg ggc tcc cgg cgc ttc cag cca gcc ctg ctc gac cta 629

Leu Pro Asn Leu Gly Ser Arg Arg Phe Gln Pro Ala Leu Leu Asp Leu

105

110

115

tcc acc gtg gag gac cac aac act cag tac ttc aac ttc gtg gag ctg 677

Ser Thr Val Glu Asp His Asn Thr Gln Tyr Phe Asn Phe Val Glu Leu

120

125

130

135

cct gct gct gcc ctg cgc ttc atg ccc aag ccg gtg ttc gtg cca gac 725

Pro Ala Ala Ala Leu Arg Phe Met Pro Lys Pro Val Phe Val Pro Asp

140

145

150

gtg gcc ctc atc gcc aac cgc ttc aac ccc gac aac ctc atg cac gtc 773

Val Ala Leu Ile Ala Asn Arg Phe Asn Pro Asp Asn Leu Met His Val

155	160	165	
ttt cat gac gac ctg ctg cca ctc ttc tac acc ctg cgg cag ttt ccc 821			
Phe His Asp Asp Leu Leu Pro Leu Phe Tyr Thr Leu Arg Gln Phe Pro			
170	175	180	
ggc ctg gcc cac gag gca cgg ctc ttc ttc atg gag ggc tgg ggc gag 869			
Gly Leu Ala His Glu Ala Arg Leu Phe Phe Met Glu Gly Trp Gly Glu			
185	190	195	
ggt gca cac ttc gac ctc tac aag ctg ctc agc ccc aag cag cct ctc 917			
Gly Ala His Phe Asp Leu Tyr Lys Leu Leu Ser Pro Lys Gln Pro Leu			
200	205	210	215
ctg cgg gca cag ctg aag acc ctg ggc cgg ctg ctg tgc ttc tcc cat 965			
Leu Arg Ala Gln Leu Lys Thr Leu Gly Arg Leu Leu Cys Phe Ser His			
220	225	230	
gct ttt gtg ggc ctc tcc aag atc act acc tgg tac cag tat ggc ttt 1013			
Ala Phe Val Gly Leu Ser Lys Ile Thr Thr Trp Tyr Gln Tyr Gly Phe			
235	240	245	
gtg cag ccc cag ggc ccg aag gcc aac atc ctc gtc tca ggc aat gag 1061			
Val Gln Pro Gln Gly Pro Lys Ala Asn Ile Leu Val Ser Gly Asn Glu			
250	255	260	
atc cgg cag ttt gca cgg ttc atg aca gaa aag ctg aac gtg agc cac 1109			
Ile Arg Gln Phe Ala Arg Phe Met Thr Glu Lys Leu Asn Val Ser His			
265	270	275	
aca gga gtc ccc cta ggc gag gag tac att ctg gtc ttt agc cga acc 1157			
Thr Gly Val Pro Leu Gly Glu Glu Tyr Ile Leu Val Phe Ser Arg Thr			
280	285	290	295
cag aac aga ctc att ctg aat gag gca gag ctg ctg ctg gca ctg gcc 1205			
Gln Asn Arg Leu Ile Leu Asn Glu Ala Glu Leu Leu Ala Leu Ala			
300	305	310	
cag gag ttc cag atg aag aca gtg aca gtg tcc ctg gag gac cac acc 1253			
Gln Glu Phe Gln Met Lys Thr Val Thr Val Ser Leu Glu Asp His Thr			
315	320	325	
ttt gct gat gtc gtg cgg ctg gtc agc aat gcc tcc atg ctg gtc agc 1301			
Phe Ala Asp Val Val Arg Leu Val Ser Asn Ala Ser Met Leu Val Ser			
330	335	340	
atg cat ggg gcc cag ctg gtc acc acc ctc ttc ctg ccc cgt ggg gca 1349			
Met His Gly Ala Gln Leu Val Thr Thr Leu Phe Leu Pro Arg Gly Ala			
345	350	355	
act gtg gta gag ctc ttc cca tat gct gtc aat ccc gac cac tac act 1397			
Thr Val Val Glu Leu Phe Pro Tyr Ala Val Asn Pro Asp His Tyr Thr			
360	365	370	375

ccc tat aag acg ctg gcc atg ctg cct ggc atg gac ctc cag tat gta 1445
 Pro Tyr Lys Thr Leu Ala Met Leu Pro Gly Met Asp Leu Gln Tyr Val
 380 385 390

gcc tgg cgg aac atg atg cca gag aac aca gtc aca cac cct gag cgg 1493
 Ala Trp Arg Asn Met Met Pro Glu Asn Thr Val Thr His Pro Glu Arg
 395 400 405

ccc tgg gat cag ggg ggc atc acc cat ctg gac cgg gct gag caa gcc 1541
 Pro Trp Asp Gln Gly Ile Thr His Leu Asp Arg Ala Glu Gln Ala
 410 415 420

cgt atc ctg caa agc cgt gag gtc cca cgg cat ctc tgt tgc cgg aac 1589
 Arg Ile Leu Gln Ser Arg Glu Val Pro Arg His Leu Cys Cys Arg Asn
 425 430 435

ccc gag tgg ctc ttc cga atc tac cag gac acc aag gtg gac atc cca 1637
 Pro Glu Trp Leu Phe Arg Ile Tyr Gln Asp Thr Lys Val Asp Ile Pro
 440 445 450 455

tcc ctc att caa acc ata cgg cgc gtg gtg aag ggc cgg cca gga cca 1685
 Ser Leu Ile Gln Thr Ile Arg Arg Val Val Lys Gly Arg Pro Gly Pro
 460 465 470

cgg aag cag aag tgg aca gtc ggc cta tat cca ggc aag gtg cgg gag 1733
 Arg Lys Gln Lys Trp Thr Val Gly Leu Tyr Pro Gly Lys Val Arg Glu
 475 480 485

gca cgg tgc cag gcg tca gtg cat ggc gcc tcc gag gcc cgc ctc act 1781
 Ala Arg Cys Gln Ala Ser Val His Gly Ala Ser Glu Ala Arg Leu Thr
 490 495 500

gtc tcc tgg cag atc cca tgg aac ctt aaa tac ctg aag gtg agg gag 1829
 Val Ser Trp Gln Ile Pro Trp Asn Leu Lys Tyr Leu Lys Val Arg Glu
 505 510 515

gtg aag tac gag gtg tgg ctg cag gag cag ggg gag aac acc tac gtg 1877
 Val Lys Tyr Glu Val Trp Leu Gln Glu Gln Gly Glu Asn Thr Tyr Val
 520 525 530 535

cct tac atc ctg gct ctg cag aac cac acc ttc act gag aac atc aag 1925
 Pro Tyr Ile Leu Ala Leu Gln Asn His Thr Phe Thr Glu Asn Ile Lys
 540 545 550

ccc ttc acc acc tac ctg gtg tgg gtc cgc tgc atc ttc aac aag atc 1973
 Pro Phe Thr Thr Tyr Leu Val Trp Val Arg Cys Ile Phe Asn Lys Ile
 555 560 565

ctc ctg gga ccc ttt gca gat gtg ctg gtg tgc aac acg tagcgagcag 2022
 Leu Leu Gly Pro Phe Ala Asp Val Leu Val Cys Asn Thr
 570 575 580

gccacagcct ggcctcggga aggtggctcc tgcagttcag cgtccctggg cccattaatc 2082
 ccactgtgga gacttctggg aactatttat tgagcaggcc tgtgcctcca catcatcttg 2142
 ttgtctctgg ggtgtggtgt cacagcactc ctcttgccc tagagataag ggacctgact 2202
 tcccttctc ccatcctgaa catttgacc cctggagaag ttccttagca gggaggagga 2262
 agaggagagg aggaagcaaa gaatcacaag gaacctctgg ctaggtgatc ctgatgttc 2322
 ctactgagtt tttctggtat ccagatttct ggaaccgcg taatcatgta ctgtttgatt 2382
 ggggtggtca tctgcttcca tccagtgaa attacctgt agcccagtga aggggtgtgt 2442
 tggaacattc attaaatgat tctaagcgaa aaaaaa 2478

<210> 10
 <211> 580
 <212> PRT
 <213> Homo sapiens

<400> 10
 Met His Leu Ser Ala Val Phe Asn Ala Leu Leu Val Ser Val Leu Ala
 1 5 10 15
 Ala Val Leu Trp Lys His Val Arg Leu Arg Glu His Ala Ala Thr Leu
 20 25 30
 Glu Glu Glu Leu Ala Leu Ser Arg Gln Ala Thr Glu Pro Ala Pro Ala
 35 40 45
 Leu Arg Ile Asp Tyr Pro Lys Ala Leu Gln Ile Leu Met Glu Gly Gly
 50 55 60
 Thr His Met Val Cys Thr Gly Arg Thr His Thr Asp Arg Ile Cys Arg
 65 70 75 80
 Phe Lys Trp Leu Cys Tyr Ser Asn Glu Ala Glu Glu Phe Ile Phe Phe
 85 90 95
 His Gly Asn Thr Ser Val Met Leu Pro Asn Leu Gly Ser Arg Arg Phe
 100 105 110
 Gln Pro Ala Leu Leu Asp Leu Ser Thr Val Glu Asp His Asn Thr Gln
 115 120 125
 Tyr Phe Asn Phe Val Glu Leu Pro Ala Ala Ala Leu Arg Phe Met Pro
 130 135 140
 Lys Pro Val Phe Val Pro Asp Val Ala Leu Ile Ala Asn Arg Phe Asn
 145 150 155 160

Pro Asp Asn Leu Met His Val Phe His Asp Asp Leu Leu Pro Leu Phe
165 170 175

Tyr Thr Leu Arg Gln Phe Pro Gly Leu Ala His Glu Ala Arg Leu Phe
180 185 190

Phe Met Glu Gly Trp Gly Glu Gly Ala His Phe Asp Leu Tyr Lys Leu
195 200 205

Leu Ser Pro Lys Gln Pro Leu Leu Arg Ala Gln Leu Lys Thr Leu Gly
210 215 220

Arg Leu Leu Cys Phe Ser His Ala Phe Val Gly Leu Ser Lys Ile Thr
225 230 235 240

Thr Trp Tyr Gln Tyr Gly Phe Val Gln Pro Gln Gly Pro Lys Ala Asn
245 250 255

Ile Leu Val Ser Gly Asn Glu Ile Arg Gln Phe Ala Arg Phe Met Thr
260 265 270

Glu Lys Leu Asn Val Ser His Thr Gly Val Pro Leu Gly Glu Glu Tyr
275 280 285

Ile Leu Val Phe Ser Arg Thr Gln Asn Arg Leu Ile Leu Asn Glu Ala
290 295 300

Glu Leu Leu Leu Ala Leu Ala Gln Glu Phe Gln Met Lys Thr Val Thr
305 310 315 320

Val Ser Leu Glu Asp His Thr Phe Ala Asp Val Val Arg Leu Val Ser
325 330 335

Asn Ala Ser Met Leu Val Ser Met His Gly Ala Gln Leu Val Thr Thr
340 345 350

Leu Phe Leu Pro Arg Gly Ala Thr Val Val Glu Leu Phe Pro Tyr Ala
355 360 365

Val Asn Pro Asp His Tyr Thr Pro Tyr Lys Thr Leu Ala Met Leu Pro
370 375 380

Gly Met Asp Leu Gln Tyr Val Ala Trp Arg Asn Met Met Pro Glu Asn
385 390 395 400

Thr Val Thr His Pro Glu Arg Pro Trp Asp Gln Gly Ile Thr His
405 410 415

Leu Asp Arg Ala Glu Gln Ala Arg Ile Leu Gln Ser Arg Glu Val Pro
420 425 430

Arg His Leu Cys Cys Arg Asn Pro Glu Trp Leu Phe Arg Ile Tyr Gln
435 440 445

Asp Thr Lys Val Asp Ile Pro Ser Leu Ile Gln Thr Ile Arg Arg Val
450 455 460

Val Lys Gly Arg Pro Gly Pro Arg Lys Gln Lys Trp Thr Val Gly Leu
465 470 475 480

Tyr Pro Gly Lys Val Arg Glu Ala Arg Cys Gln Ala Ser Val His Gly
485 490 495

Ala Ser Glu Ala Arg Leu Thr Val Ser Trp Gln Ile Pro Trp Asn Leu
500 505 510

Lys Tyr Leu Lys Val Arg Glu Val Lys Tyr Glu Val Trp Leu Gln Glu
515 520 525

Gln Gly Glu Asn Thr Tyr Val Pro Tyr Ile Leu Ala Leu Gln Asn His
530 535 540

Thr Phe Thr Glu Asn Ile Lys Pro Phe Thr Thr Tyr Leu Val Trp Val
545 550 555 560

Arg Cys Ile Phe Asn Lys Ile Leu Leu Gly Pro Phe Ala Asp Val Leu
565 570 575

Val Cys Asn Thr
580

<210> 11
<211> 523
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (141)..(503)

<400> 11
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tttacgacct acagatttag gccctgattc tcttctttt caggaatgtg cacctcacct 120

tgttctccca gacctgggg atg aag gaa aca gga gcc tca ccc agg agg ctc 173
Met Lys Glu Thr Gly Ala Ser Pro Arg Arg Leu
1 5 10

aag gcc aaa act ctg acc caa act acc tca gga gcc cct ggc cct ggc 221
Lys Ala Lys Thr Leu Thr Thr Thr Ser Gly Ala Pro Gly Pro Gly
15 20 25

ttc ccc cct gct cca gag ttt ctg ccc tgc cca cac aca cac acc ctc 269

Phe Pro Pro Ala Pro Glu Phe Leu Pro Cys Pro His Thr His Thr Leu
30 35 40

ttc cac cct cag agg ccc cgg tgt cct gcc cca cgc tct acc cca gag 317
Phe His Pro Gln Arg Pro Arg Cys Pro Ala Pro Arg Ser Thr Pro Glu
45 50 55

ccc cac ggg tgg ctt tat aaa agt gcc ggg ccc agc cct cta gca gga 365
Pro His Gly Trp Leu Tyr Lys Ser Ala Gly Pro Ser Pro Leu Ala Gly
60 65 70 75

ggg gaa tgc tgg gca tct ggg tgt ggg acc ccc ggg gaa cag cct gtg 413
Gly Glu Cys Trp Ala Ser Gly Cys Gly Thr Pro Gly Glu Gln Pro Val
80 85 90

gtc tgg act cct gca tct atg agg gga cag acg tgg ctt ccc ttc cgg 461
Val Trp Thr Pro Ala Ser Met Arg Gly Gln Thr Trp Leu Pro Phe Arg
95 100 105

atg atg ggg tac cca cag atg atg gag gcc agg gtc cct caa 503
Met Met Gly Tyr Pro Gln Met Met Glu Ala Arg Val Pro Gln
110 115 120

taaaagaagg ggtgcaaaaa 523

<210> 12
<211> 121
<212> PRT
<213> Homo sapiens

<400> 12
Met Lys Glu Thr Gly Ala Ser Pro Arg Arg Leu Lys Ala Lys Thr Leu
1 5 10 15

Thr Gln Thr Thr Ser Gly Ala Pro Gly Pro Gly Phe Pro Pro Ala Pro
20 25 30

Glu Phe Leu Pro Cys Pro His Thr His Thr Leu Phe His Pro Gln Arg
35 40 45

Pro Arg Cys Pro Ala Pro Arg Ser Thr Pro Glu Pro His Gly Trp Leu
50 55 60

Tyr Lys Ser Ala Gly Pro Ser Pro Leu Ala Gly Gly Glu Cys Trp Ala
65 70 75 80

Ser Gly Cys Gly Thr Pro Gly Glu Gln Pro Val Val Trp Thr Pro Ala
85 90 95

Ser Met Arg Gly Gln Thr Trp Leu Pro Phe Arg Met Met Gly Tyr Pro
100 105 110

Gln Met Met Glu Ala Arg Val Pro Gln
115 120

<210> 13
<211> 3863
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (178)..(3156)

<220>
<223> n 1755 can be A, G, C, or T

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ctgcggcccc gctccctcta cccggccgga cccggctctg cccccgcgcc caagccccac 120
caagcccccc gccctccgcg cgcggtccca gccagggcg cgcccgcaac cagcacc 177

atg cgc ccg gta gcc ctg ctg ctc ctg ccc tcg ctg ctg gcg ctc ctg 225
Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu
1 5 10 15

gct cac gga ctc tct tta gag gcc cca acc gtg ggg aaa gga caa gcc 273
Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala
20 25 30

cca ggc atc gag gag aca gat ggc gag ctg aca gca gcc ccc aca cct 321
Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro
35 40 45

gag cag cca gaa cga ggc gtc cac ttt gtc aca aca gcc ccc acc ttg 369
Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu
50 55 60

aag ctg ctc aac cac cac ccg ctg ctt gag gaa ttc cta caa gag ggg 417
Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly
65 70 75 80

ctg gaa aag gga gat gag gag ctg agg cca gca ctg ccc ttc cag cct 465
Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro
85 90 95

gac cca cct gca ccc ttc acc cca agt ccc ctt ccc cgc ctg gcc aac 513
Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn
100 105 110

cag gac agc cgc cct gtc ttt acc agc ccc act cca gcc atg gct gcg 561

Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala
115 120 125

gta ccc act cag ccc cag tcc aag gag gga ccc tgg agt ccg gag tca 609
Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser
130 135 140

gag tcc cct atg ctt cga atc aca gct ccc cta cct cca ggg ccc agc 657
Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser
145 150 155 160

atg gca gtg ccc acc cta ggc cca ggg gag ata gcc agc act aca ccc 705
Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro
165 170 175

ccc agc aga gcc tgg aca cca acc caa gag ggt cct gga gac atg gga 753
Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly
180 185 190

agg ccg tgg gtt gca gag gtt gtg tcc cag ggc gca ggg atc ggg atc 801
Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile
195 200 205

cag ggg acc atc acc tcc tcc aca gct tca gga gat gat gag gag acc 849
Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr
210 215 220

acc act acc acc acc atc atc acc acc acc atc acc aca gtc cag aca 897
Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Thr Thr Val Gln Thr
225 230 235 240

cca ggc cct tgt agc tgg aat ttc tca ggc cca gag ggc tct ctg gac 945
Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp
245 250 255

tcc cct aca gac ctc agc tcc ccc act gat gtt ggc ctg gac tgc ttc 993
Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe
260 265 270

ttc tac atc tct gtc tac cct ggc tat ggc gtg gaa atc aag gtc cag 1041
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln
275 280 285

aat atc agc ctc cgg gaa ggg gag aca gtg act gtg gaa ggc ctg ggg 1089
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly
290 295 300

ggg cct gac cca ctg ccc ctg gcc aac cag tct ttc ctg ctg cgg ggc 1137
Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly
305 310 315 320

caa gtc atc cgc agc ccc acc cac caa gcg gcc ctg agg ttc cag agc 1185
Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser

325	330	335	
ctc ccg cca ccg gct ggc cct ggc acc ttc cat ttc cat tac caa gcc 1233			
Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala			
340	345	350	
tat ctc ctg agc tgc cac ttt ccc cgt cgt caa gct tat gaa gat gtg 1281			
Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Gln Ala Tyr Glu Asp Val			
355	360	365	
act gtc acc agc atc cac cca gga ggt agt gcc cgc ttc cat tgt gca 1329			
Thr Val Thr Ser Ile His Pro Gly Gly Ser Ala Arg Phe His Cys Ala			
370	375	380	
act ggc tac cag ctg aag ggc gcc agg cat ctc acc tgt ctc aat gcc 1377			
Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala			
385	390	395	400
acc cag ccc atc tgg gat tca aag gag ccc gta tgc atc gct gct tgc 1425			
Thr Gln Pro Ile Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys			
405	410	415	
ggc gga gtg atc cgc aat gcc acc acc ggc cgc atc gtc tct cca ggc 1473			
Gly Gly Val Ile Arg Asn Ala Thr Thr Gly Arg Ile Val Ser Pro Gly			
420	425	430	
ttc ccg ggc aac tac agc aac aac ctc acc tgt cac tgg ctg ctt gag 1521			
Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu			
435	440	445	
gct cct gag ggc cag cgg cta cac ctg cac ttt gag aag gtt tcc ctg 1569			
Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu			
450	455	460	
gca gag gat gat gac agg ctc atc att cgc aat ggg gac aac gtg gag 1617			
Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu			
465	470	475	480
gcc cca cca gtg tat gat tcc tat gag gtg gaa tac ctg ccc att gag 1665			
Ala Pro Pro Val Tyr Asp Ser Tyr Glu Val Glu Tyr Leu Pro Ile Glu			
485	490	495	
ggc ctg ctc agc tct ggc aaa cac ttc ttt gtt gag ctc agt act gac 1713			
Gly Leu Leu Ser Ser Gly Lys His Phe Phe Val Glu Leu Ser Thr Asp			
500	505	510	
agc agc ggg gca gct gca ggc atg gcc ctg cgc tat gag gcn ttc cag 1761			
Ser Ser Gly Ala Ala Ala Gly Met Ala Leu Arg Tyr Glu Ala Phe Gln			
515	520	525	
cag ggc cat tgc tat gag ccc ttt gtc aaa tac ggt aac ttc agc agc 1809			
Gln Gly His Cys Tyr Glu Pro Phe Val Lys Tyr Gly Asn Phe Ser Ser			
530	535	540	

agc aca ccc acc tac cct gtg ggt acc act gtg gag ttt agc tgc gac 1857
Ser Thr Pro Thr Tyr Pro Val Gly Thr Thr Val Glu Phe Ser Cys Asp
545 550 555 560

cct ggc tac acc ctg gag cag ggc tcc atc atc atc gag tgt gtt gac 1905
Pro Gly Tyr Thr Leu Glu Gln Gly Ser Ile Ile Ile Glu Cys Val Asp
565 570 575

ccc cac gac ccc cag tgg aat gag aca gag cca gcc tgc cga gcc gtg 1953
Pro His Asp Pro Gln Trp Asn Glu Thr Glu Pro Ala Cys Arg Ala Val
580 585 590

tgc agc ggg gag atc aca gac tcg gct ggc gtg gta ctc tct ccc aac 2001
Cys Ser Gly Glu Ile Thr Asp Ser Ala Gly Val Val Leu Ser Pro Asn
595 600 605

tgg cca gag ccc tac agt cgt ggg cag gat tgt atc tgg ggt gtg cat 2049
Trp Pro Glu Pro Tyr Ser Arg Gly Gln Asp Cys Ile Trp Gly Val His
610 615 620

gtg gaa gag gac aag cgc atc atg ctg gac atc cga gtg ctg cgc ata 2097
Val Glu Glu Asp Lys Arg Ile Met Leu Asp Ile Arg Val Leu Arg Ile
625 630 635 640

ggc cct ggt gat gtg ctt acc ttc tat gat ggg gat gac ctg acg gcc 2145
Gly Pro Gly Asp Val Leu Thr Phe Tyr Asp Gly Asp Asp Leu Thr Ala
645 650 655

cgg gtt ctg ggc cag tac tca ggg ccc cgt agc cac ttc aag ctc ttt 2193
Arg Val Leu Gly Gln Tyr Ser Gly Pro Arg Ser His Phe Lys Leu Phe
660 665 670

acc tcc atg gct gat gtc acc att cag ttc cag tcg gac ccc ggg acc 2241
Thr Ser Met Ala Asp Val Thr Ile Gln Phe Gln Ser Asp Pro Gly Thr
675 680 685

tca gtg ctg ggc tac cag cag ggc ttc gtc atc cac ttc ttt gag gtg 2289
Ser Val Leu Gly Tyr Gln Gln Gly Phe Val Ile His Phe Phe Glu Val
690 695 700

ccc cgc aat gac aca tgt ccg gag ctg cct gag atc ccc aat ggc tgg 2337
Pro Arg Asn Asp Thr Cys Pro Glu Leu Pro Glu Ile Pro Asn Gly Trp
705 710 715 720

aag agc cca tcg cag cct gag cta gtg cac ggc acc gtg gtc act tac 2385
Lys Ser Pro Ser Gln Pro Glu Leu Val His Gly Thr Val Val Thr Tyr
725 730 735

cag tgc tac cct ggc tac cag gta gtg gga tcc agt gtc ctc atg tgc 2433
Gln Cys Tyr Pro Gly Tyr Gln Val Val Gly Ser Ser Val Leu Met Cys
740 745 750

cag tgg gac cta act tgg agt gag gac ctg ccc tca tgc cag agg gtg 2481
Gln Trp Asp Leu Thr Trp Ser Glu Asp Leu Pro Ser Cys Gln Arg Val
755 760 765

act tcc tgc cac gat cct gga gat gtg gag cac agc cga cgc ctc ata 2529
Thr Ser Cys His Asp Pro Gly Asp Val Glu His Ser Arg Arg Leu Ile
770 775 780

tcc agc ccc aag ttt ccc gtg ggg gcc acc gtg caa tat atc tgt gac 2577
Ser Ser Pro Lys Phe Pro Val Gly Ala Thr Val Gln Tyr Ile Cys Asp
785 790 795 800

cag ggt ttt gtg ctg acg ggc agc tcc atc ctc acc tgc cat gat cgc 2625
Gln Gly Phe Val Leu Thr Gly Ser Ser Ile Leu Thr Cys His Asp Arg
805 810 815

cag gct ggc agc ccc aag tgg agt gac cgg gcc cct aaa tgt ctc ctg 2673
Gln Ala Gly Ser Pro Lys Trp Ser Asp Arg Ala Pro Lys Cys Leu Leu
820 825 830

gaa cag ctc aag cca tgc cat ggt ctc agt gcc cct gag aat ggt gcc 2721
Glu Gln Leu Lys Pro Cys His Gly Leu Ser Ala Pro Glu Asn Gly Ala
835 840 845

cga agt cct gag aag cag cta cac cca gca ggg gcc acc atc cac ttc 2769
Arg Ser Pro Glu Lys Gln Leu His Pro Ala Gly Ala Thr Ile His Phe
850 855 860

tcg tgt gcc cct ggc tat gtg ctg aag ggc cag gcc agc atc aag tgt 2817
Ser Cys Ala Pro Gly Tyr Val Leu Lys Gly Gln Ala Ser Ile Lys Cys
865 870 875 880

gtg cct ggg cac ccc tcg cat tgg agt gac ccc cca ccc atc tgt agg 2865
Val Pro Gly His Pro Ser His Trp Ser Asp Pro Pro Pro Ile Cys Arg
885 890 895

gct gcc tct ctg gat ggg ttc tac aac agt cgc agc ctg gat gtt gcc 2913
Ala Ala Ser Leu Asp Gly Phe Tyr Asn Ser Arg Ser Leu Asp Val Ala
900 905 910

aag gca cct gct gcc tcc agc acc ctg gat gct gcc cac att gca gct 2961
Lys Ala Pro Ala Ala Ser Ser Thr Leu Asp Ala Ala His Ile Ala Ala
915 920 925

gcc atc ttc ttg cca ctg gtg gcg atg gtg ttg ttg gta gga ggt gta 3009
Ala Ile Phe Leu Pro Leu Val Ala Met Val Leu Leu Val Gly Gly Val
930 935 940

tac ttc tac ttc tcc agg ctc cag gga aaa agc tcc ctg cag ctg ccc 3057
Tyr Phe Tyr Phe Ser Arg Leu Gln Gly Lys Ser Ser Leu Gln Leu Pro
945 950 955 960

cgc ccc cgc ccc cgc ccc tac aac cgc att acc ata gag tca gcg ttt 3105

Arg Pro Arg Pro Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe
 965 970 975

gac aat cca act tac gag act gga gag acg aga gaa tat gaa gtc tcc 3153
 Asp Asn Pro Thr Tyr Glu Thr Gly Glu Thr Arg Glu Tyr Glu Val Ser
 980 985 990

atc taggtggggg cagtctaggg aagtcaactc agacttcac cacagtccag 3206
 Ile

cagcaaggct ccttgcttcc tgctgtccct ccacctctg tatataccac ctaggaggag 3266

atgccaccaa gccctcaaga agttgtgccc tccccgcct gcgatgccca ccatggccta 3326

ttttcttggg gtcaattgccc acttggggcc cttcattggg cccatgtcag ggggcatcta 3386

cctgtgggaa gaacatagct ggagcacaag catcaacagc cagcatcctg agcctctca 3446

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ggtagtctg gcatgccaac atcagcctct tgggaggtct ctagtctct aaagttctgg 3686

acagttctgc ctctgacct gtcccagtg aggcagtaat tctaggagat cctaaggggt 3746

tcagggggac cctaccccca cctcaggttg ggcttcctg ggcactcatg ctccacacca 3806

aagcaggaca cgccatttct cactgaccac cctataccct gaggaagggt agacttt 3863

<210> 14

<211> 993

<212> PRT

<213> Homo sapiens

<223> n 1755 can be A, G, C, or T

<400> 14

Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu
 1 5 10 15

Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala
 20 25 30

Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro
 35 40 45

Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu
 50 55 60

Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly

65	70	75	80
Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro			
	85	90	95
Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn			
	100	105	110
Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala			
	115	120	125
Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser			
	130	135	140
Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser			
	145	150	155
		160	
Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro			
	165	170	175
Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly			
	180	185	190
Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile			
	195	200	205
Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr			
	210	215	220
Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr			
	225	230	235
		240	
Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp			
	245	250	255
Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe			
	260	265	270
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln			
	275	280	285
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly			
	290	295	300
Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly			
	305	310	315
		320	
Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser			
	325	330	335
Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala			
	340	345	350

Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Gln Ala Tyr Glu Asp Val
355 360 365

Thr Val Thr Ser Ile His Pro Gly Gly Ser Ala Arg Phe His Cys Ala
370 375 380

Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala
385 390 395 400

Thr Gln Pro Ile Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys
405 410 415

Gly Gly Val Ile Arg Asn Ala Thr Thr Gly Arg Ile Val Ser Pro Gly
420 425 430

Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu
435 440 445

Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu
450 455 460

Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu
465 470 475 480

Ala Pro Pro Val Tyr Asp Ser Tyr Glu Val Glu Tyr Leu Pro Ile Glu
485 490 495

Gly Leu Leu Ser Ser Gly Lys His Phe Phe Val Glu Leu Ser Thr Asp
500 505 510

Ser Ser Gly Ala Ala Ala Gly Met Ala Leu Arg Tyr Glu Ala Phe Gln
515 520 525

Gln Gly His Cys Tyr Glu Pro Phe Val Lys Tyr Gly Asn Phe Ser Ser
530 535 540

Ser Thr Pro Thr Tyr Pro Val Gly Thr Thr Val Glu Phe Ser Cys Asp
545 550 555 560

Pro Gly Tyr Thr Leu Glu Gln Gly Ser Ile Ile Ile Glu Cys Val Asp
565 570 575

Pro His Asp Pro Gln Trp Asn Glu Thr Glu Pro Ala Cys Arg Ala Val
580 585 590

Cys Ser Gly Glu Ile Thr Asp Ser Ala Gly Val Val Leu Ser Pro Asn
595 600 605

Trp Pro Glu Pro Tyr Ser Arg Gly Gln Asp Cys Ile Trp Gly Val His
610 615 620

Val Glu Glu Asp Lys Arg Ile Met Leu Asp Ile Arg Val Leu Arg Ile
625 630 635 640

Gly Pro Gly Asp Val Leu Thr Phe Tyr Asp Gly Asp Asp Leu Thr Ala
645 650 655

Arg Val Leu Gly Gln Tyr Ser Gly Pro Arg Ser His Phe Lys Leu Phe
660 665 670

Thr Ser Met Ala Asp Val Thr Ile Gln Phe Gln Ser Asp Pro Gly Thr
675 680 685

Ser Val Leu Gly Tyr Gln Gln Gly Phe Val Ile His Phe Phe Glu Val
690 695 700

Pro Arg Asn Asp Thr Cys Pro Glu Leu Pro Glu Ile Pro Asn Gly Trp
705 710 715 720

Lys Ser Pro Ser Gln Pro Glu Leu Val His Gly Thr Val Val Thr Tyr
725 730 735

Gln Cys Tyr Pro Gly Tyr Gln Val Val Gly Ser Ser Val Leu Met Cys
740 745 750

Gln Trp Asp Leu Thr Trp Ser Glu Asp Leu Pro Ser Cys Gln Arg Val
755 760 765

Thr Ser Cys His Asp Pro Gly Asp Val Glu His Ser Arg Arg Leu Ile
770 775 780

Ser Ser Pro Lys Phe Pro Val Gly Ala Thr Val Gln Tyr Ile Cys Asp
785 790 795 800

Gln Gly Phe Val Leu Thr Gly Ser Ser Ile Leu Thr Cys His Asp Arg
805 810 815

Gln Ala Gly Ser Pro Lys Trp Ser Asp Arg Ala Pro Lys Cys Leu Leu
820 825 830

Glu Gln Leu Lys Pro Cys His Gly Leu Ser Ala Pro Glu Asn Gly Ala
835 840 845

Arg Ser Pro Glu Lys Gln Leu His Pro Ala Gly Ala Thr Ile His Phe
850 855 860

Ser Cys Ala Pro Gly Tyr Val Leu Lys Gly Gln Ala Ser Ile Lys Cys
865 870 875 880

Val Pro Gly His Pro Ser His Trp Ser Asp Pro Pro Pro Ile Cys Arg
885 890 895

Ala Ala Ser Leu Asp Gly Phe Tyr Asn Ser Arg Ser Leu Asp Val Ala
900 905 910

Lys Ala Pro Ala Ala Ser Ser Thr Leu Asp Ala Ala His Ile Ala Ala

915	920	925
Ala Ile Phe Leu Pro Leu Val Ala Met Val Leu Leu Val Gly Gly Val		
930	935	940
Tyr Phe Tyr Phe Ser Arg Leu Gln Gly Lys Ser Ser Leu Gln Leu Pro		
945	950	955 960
Arg Pro Arg Pro Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe		
965	970	975
Asp Asn Pro Thr Tyr Glu Thr Gly Glu Thr Arg Glu Tyr Glu Val Ser		
980	985	990

Ile

<210> 15
 <211> 3879
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (178)..(3159)

<220>
 <223> n 1755 can be A, G, C, or T.

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 caagcccccc gccctccgc cgcggtcca gccagggcg cgccgcaac cagcacc 177
 atg cgc ccg gta gcc ctg ctg ctc ctg ccc tcg ctg ctg gcg ctc ctg 225
 Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu
 1 5 10 15
 gct cac gga ctc tct tta gag gcc cca acc gtg ggg aaa gga caa gcc 273
 Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala
 20 25 30
 cca ggc atc gag gag aca gat ggc gag ctg aca gca gcc ccc aca cct 321
 Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro
 35 40 45
 gag cag cca gaa cga ggc gtc cac ttt gtc aca aca gcc ccc acc ttg 369
 Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu
 50 55 60

aag ctg ctc aac cac cac ccg ctg ctt gag gaa ttc cta caa gag ggg 417
 Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly
 65 70 75 80

ctg gaa aag gga gat gag gag ctg agg cca gca ctg ccc ttc cag cct 465
 Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro
 85 90 95

gac cca cct gca ccc ttc acc cca agt ccc ctt ccc cgc ctg gcc aac 513
 Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn
 100 105 110

cag gac agc cgc cct gtc ttt acc agc ccc act cca gcc atg gct gcg 561
 Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala
 115 120 125

gta ccc act cag ccc cag tcc aag gag gga ccc tgg agt ccg gag tca 609
 Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser
 130 135 140

gag tcc cct atg ctt cga atc aca gct ccc cta cct cca ggg ccc agc 657
 Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser
 145 150 155 160

atg gca gtg ccc acc cta ggc cca ggg gag ata gcc agc act aca ccc 705
 Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro
 165 170 175

ccc agc aga gcc tgg aca cca acc caa gag ggt cct gga gac atg gga 753
 Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly
 180 185 190

agg ccg tgg gtt gca gag gtt gtg tcc cag ggc gca ggg atc ggg atc 801
 Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile
 195 200 205

cag ggg acc atc acc tcc tcc aca gct tca gga gat gat gag gag acc 849
 Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr
 210 215 220

acc act acc acc acc atc atc acc acc acc atc acc aca gtc cag aca 897
 Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr
 225 230 235 240

cca ggc cct tgt agc tgg aat ttc tca ggc cca gag ggc tct ctg gac 945
 Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp
 245 250 255

tcc cct aca gac ctc agc tcc ccc act gat gtt ggc ctg gac tgc ttc 993
 Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe
 260 265 270

ttc tac atc tct gtc tac cct ggc tat ggc gtg gaa atc aag gtc cag 1041
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln
275 280 285

aat atc agc ctc cgg gaa ggg gag aca gtg act gtg gaa ggc ctg ggg 1089
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly
290 295 300

ggg cct gac cca ctg ccc ctg gcc aac cag tct ttc ctg ctg cgg ggc 1137
Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly
305 310 315 320

caa gtc atc cgc agc ccc acc cac caa gcg gcc ctg agg ttc cag agc 1185
Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser
325 330 335

ctc ccg cca ccg gct ggc cct ggc acc ttc cat ttc cat tac caa gcc 1233
Leu Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala
340 345 350

tat ctc ctg agc tgc cac ttt ccc cgt cgt caa gct tat gaa gat gtg 1281
Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Gln Ala Tyr Glu Asp Val
355 360 365

act gtc acc agc atc cac cca gga ggt agt gcc cgc ttc cat tgt gca 1329
Thr Val Thr Ser Ile His Pro Gly Gly Ser Ala Arg Phe His Cys Ala
370 375 380

act ggc tac cag ctg aag ggc gcc agg cat ctc acc tgt ctc aat gcc 1377
Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala
385 390 395 400

acc cag ccc atc tgg gat tca aag gag ccc gta tgc atc gct gct tgc 1425
Thr Gln Pro Ile Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys
405 410 415

ggc gga gtg atc cgc aat gcc acc acc ggc cgc atc gtc tct cca ggc 1473
Gly Gly Val Ile Arg Asn Ala Thr Thr Gly Arg Ile Val Ser Pro Gly
420 425 430

ttc ccg ggc aac tac agc aac aac ctc acc tgt cac tgg ctg ctt gag 1521
Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu
435 440 445

gct cct gag ggc cag cgg cta cac ctg cac ttt gag aag gtt tcc ctg 1569
Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu
450 455 460

gca gag gat gat gac agg ctc atc att cgc aat ggg gac aac gtg gag 1617
Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu
465 470 475 480

gcc cca cca gtg tat gat tcc tat gag gtg gaa tac ctg ccc att gag 1665

Ala Pro Pro Val Tyr Asp Ser Tyr Glu Val Glu Tyr Leu Pro Ile Glu
485 490 495

ggc ctg ctc agc tct ggc aaa cac ttc ttt gtt gag ctc agt act gac 1713
Gly Leu Leu Ser Ser Gly Lys His Phe Phe Val Glu Leu Ser Thr Asp
500 505 510

agc agc ggg gca gct gca ggc atg gcc ctg cgc tat gag gcn ttc cag 1761
Ser Ser Gly Ala Ala Ala Gly Met Ala Leu Arg Tyr Glu Ala Phe Gln
515 520 525

cag ggc cat tgc tat gag ccc ttt gtc aaa tac ggt aac ttc agc agc 1809
Gln Gly His Cys Tyr Glu Pro Phe Val Lys Tyr Gly Asn Phe Ser Ser
530 535 540

agc aca ccc acc tac cct gtg ggt acc act gtg gag ttt agc tgc gac 1857
Ser Thr Pro Thr Tyr Pro Val Gly Thr Thr Val Glu Phe Ser Cys Asp
545 550 555 560

cct ggc tac acc ctg gag cag ggc tcc atc atc atc gag tgt gtt gac 1905
Pro Gly Tyr Thr Leu Glu Gln Gly Ser Ile Ile Ile Glu Cys Val Asp
565 570 575

ccc cac gac ccc cag tgg aat gag aca gag cca gcc tgc cga gcc gtg 1953
Pro His Asp Pro Gln Trp Asn Glu Thr Glu Pro Ala Cys Arg Ala Val
580 585 590

tgc agc ggg gag atc aca gac tcg gct ggc gtg gta ctc tct ccc aac 2001
Cys Ser Gly Glu Ile Thr Asp Ser Ala Gly Val Val Leu Ser Pro Asn
595 600 605

tgg cca gag ccc tac agt cgt ggg cag gat tgt atc tgg ggt gtg cat 2049
Trp Pro Glu Pro Tyr Ser Arg Gly Gln Asp Cys Ile Trp Gly Val His
610 615 620

gtg gaa gag gac aag cgc atc atg ctg gac atc cga gtg ctg cgc ata 2097
Val Glu Glu Asp Lys Arg Ile Met Leu Asp Ile Arg Val Leu Arg Ile
625 630 635 640

ggc cct ggt gat gtg ctt acc ttc tat gat ggg gat gac ctg acg gcc 2145
Gly Pro Gly Asp Val Leu Thr Phe Tyr Asp Gly Asp Asp Leu Thr Ala
645 650 655

cgg gtt ctg ggc cag tac tca ggg ccc cgt agc cac ttc aag ctc ttt 2193
Arg Val Leu Gly Gln Tyr Ser Gly Pro Arg Ser His Phe Lys Leu Phe
660 665 670

acc tcc atg gct gat gtc acc att cag ttc cag tcg gac ccc ggg acc 2241
Thr Ser Met Ala Asp Val Thr Ile Gln Phe Gln Ser Asp Pro Gly Thr
675 680 685

tca gtg ctg ggc tac cag cag ggc ttc gtc atc cac ttc ttt gag gtg 2289
Ser Val Leu Gly Tyr Gln Gln Gly Phe Val Ile His Phe Phe Glu Val

690	695	700	
ccc cgc aat gac aca tgt ccg gag ctg cct gag atc ccc aat ggc tgg	2337		
Pro Arg Asn Asp Thr Cys Pro Glu Leu Pro Glu Ile Pro Asn Gly Trp			
705	710	715	720
aag agc cca tcg cag cct gag cta gtg cac ggc acc gtg gtc act tac	2385		
Lys Ser Pro Ser Gln Pro Glu Leu Val His Gly Thr Val Val Thr Tyr			
725	730	735	
cag tgc tac cct ggc tac cag gta gtg gga tcc agt gtc ctc atg tgc	2433		
Gln Cys Tyr Pro Gly Tyr Gln Val Val Gly Ser Ser Val Leu Met Cys			
740	745	750	
cag tgg gac cta act tgg agt gag gac ctg ccc tca tgc cag agg gtg	2481		
Gln Trp Asp Leu Thr Trp Ser Glu Asp Leu Pro Ser Cys Gln Arg Val			
755	760	765	
act tcc tgc cac gat cct gga gat gtg gag cac agc cga cgc ctc ata	2529		
Thr Ser Cys His Asp Pro Gly Asp Val Glu His Ser Arg Arg Leu Ile			
770	775	780	
tcc agc ccc aag ttt ccc gtg ggg gcc acc gtg caa tat atc tgt gac	2577		
Ser Ser Pro Lys Phe Pro Val Gly Ala Thr Val Gln Tyr Ile Cys Asp			
785	790	795	800
cag ggt ttt gtg ctg acg ggc agc tcc atc ctc acc tgc cat gat cgc	2625		
Gln Gly Phe Val Leu Thr Gly Ser Ser Ile Leu Thr Cys His Asp Arg			
805	810	815	
cag gct ggc agc ccc aag tgg agt gac cgg gcc cct aaa tgt ctc ctg	2673		
Gln Ala Gly Ser Pro Lys Trp Ser Asp Arg Ala Pro Lys Cys Leu Leu			
820	825	830	
gaa cag ctc aag cca tgc cat ggt ctc agt gcc cct gag aat ggt gcc	2721		
Glu Gln Leu Lys Pro Cys His Gly Leu Ser Ala Pro Glu Asn Gly Ala			
835	840	845	
cga agt cct gag aag cag cta cac cca gca ggg gcc acc atc cac ttc	2769		
Arg Ser Pro Glu Lys Gln Leu His Pro Ala Gly Ala Thr Ile His Phe			
850	855	860	
tcg tgt gcc cct ggc tat gtg ctg aag ggc cag gcc agc atc aag tgt	2817		
Ser Cys Ala Pro Gly Tyr Val Leu Lys Gly Gln Ala Ser Ile Lys Cys			
865	870	875	880
gtg cct ggg cac ccc tcg cat tgg agt gac ccc cca ccc atc tgt agg	2865		
Val Pro Gly His Pro Ser His Trp Ser Asp Pro Pro Pro Ile Cys Arg			
885	890	895	
gct gcc tct ctg gat ggg ttc tac aac agt cgc agc ctg gat gtt gcc	2913		
Ala Ala Ser Leu Asp Gly Phe Tyr Asn Ser Arg Ser Leu Asp Val Ala			
900	905	910	

aag gca cct gct gcc tcc agc acc ctg gat gct gcc cac att gca gct 2961
 Lys Ala Pro Ala Ala Ser Ser Thr Leu Asp Ala Ala His Ile Ala Ala
 915 920 925

gcc atc ttc ttg cca ctg gtg gcg atg gtg ttg gta gga ggt gta 3009
 Ala Ile Phe Leu Pro Leu Val Ala Met Val Leu Leu Val Gly Gly Val
 930 935 940

tac ttc tac ttc tcc agg ctc cag gga aaa agc tcc ctg cag ctg ccc 3057
 Tyr Phe Tyr Phe Ser Arg Leu Gln Gly Lys Ser Ser Leu Gln Leu Pro
 945 950 955 960

cgc ccc cgc ccc cgc ccc tac aac cgc att acc ata gag tca gcg ttt 3105
 Arg Pro Arg Pro Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe
 965 970 975

gac aat cca act tac gag act gga tct ctt tcc ttt gca gga gac gag 3153
 Asp Asn Pro Thr Tyr Glu Thr Gly Ser Leu Ser Phe Ala Gly Asp Glu
 980 985 990

aga ata tgaagtctcc atctaggtgg gggcagtcta gggaagtcaa ctcagacttg 3209
 Arg Ile

caccacagtc cagcagcaag gctccttgct tctgtctgtc cctccacctc ctgtatatac 3269

cacctaggag gagatgccac caagccctca agaagttgtg cccttccccg cctgcgatgc 3329

ccaccatggc ctattttctt ggtgtcattg cccacttggg gcccttcatt gggcccatgt 3389

cagggggcat ctacctgtgg gaagaacata gctggagcac aagcatcaac agccagcatc 3449

ctgagcctcc tcatgccctg gaccagcctg gaacacacta gcagagcagg agtacctttc 3509

tccacatgac caccatcccc ccctggcatg gcaacctgca gcaggattaa cttgacatg 3569

gtgggaactg caccagggtg ctctcacag cgccatcacc aatggccaaa actcctctca 3629

acggtgacct ctgggtagtc ctggcatgcc aacatcagcc tcttgggagg tcttagttc 3689

tctaaagttc tggacagttc tgctctctgc cctgtcccag tggaggcagt aattctagga 3749

gatcctaagg gggtcagggg gaccctaccc ccacctcagg ttgggcttcc ctgggcactc 3809

atgctccaca ccaaagcagg acacgccatt ttccactgac caccctatac cctgaggaaa 3869

gggagacttt 3879

<210> 16

<211> 994

<212> PRT

<213> Homo sapiens

<223> n 1755 can be A, G, C, or T.

<400> 16

Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu
1 5 10 15

Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala
20 25 30

Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro
35 40 45

Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu
50 55 60

Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly
65 70 75 80

Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro
85 90 95

Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn
100 105 110

Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala
115 120 125

Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser
130 135 140

Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser
145 150 155 160

Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro
165 170 175

Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly
180 185 190

Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile
195 200 205

Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr
210 215 220

Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr
225 230 235 240

Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp
245 250 255

Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe
260 265 270

Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln
275 280 285

Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly
290 295 300

Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly
305 310 315 320

Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser
325 330 335

Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala
340 345 350

Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Gln Ala Tyr Glu Asp Val
355 360 365

Thr Val Thr Ser Ile His Pro Gly Gly Ser Ala Arg Phe His Cys Ala
370 375 380

Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala
385 390 395 400

Thr Gln Pro Ile Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys
405 410 415

Gly Gly Val Ile Arg Asn Ala Thr Thr Gly Arg Ile Val Ser Pro Gly
420 425 430

Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu
435 440 445

Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu
450 455 460

Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu
465 470 475 480

Ala Pro Pro Val Tyr Asp Ser Tyr Glu Val Glu Tyr Leu Pro Ile Glu
485 490 495

Gly Leu Leu Ser Ser Gly Lys His Phe Phe Val Glu Leu Ser Thr Asp
500 505 510

Ser Ser Gly Ala Ala Ala Gly Met Ala Leu Arg Tyr Glu Ala Phe Gln
515 520 525

Gln Gly His Cys Tyr Glu Pro Phe Val Lys Tyr Gly Asn Phe Ser Ser
530 535 540

Ser Thr Pro Thr Tyr Pro Val Gly Thr Thr Val Glu Phe Ser Cys Asp

545	550	555	560
Pro Gly Tyr Thr Leu Glu Gln Gly Ser Ile Ile Ile Glu Cys Val Asp			
565	570	575	
Pro His Asp Pro Gln Trp Asn Glu Thr Glu Pro Ala Cys Arg Ala Val			
580	585	590	
Cys Ser Gly Glu Ile Thr Asp Ser Ala Gly Val Val Leu Ser Pro Asn			
595	600	605	
Trp Pro Glu Pro Tyr Ser Arg Gly Gln Asp Cys Ile Trp Gly Val His			
610	615	620	
Val Glu Glu Asp Lys Arg Ile Met Leu Asp Ile Arg Val Leu Arg Ile			
625	630	635	640
Gly Pro Gly Asp Val Leu Thr Phe Tyr Asp Gly Asp Asp Leu Thr Ala			
645	650	655	
Arg Val Leu Gly Gln Tyr Ser Gly Pro Arg Ser His Phe Lys Leu Phe			
660	665	670	
Thr Ser Met Ala Asp Val Thr Ile Gln Phe Gln Ser Asp Pro Gly Thr			
675	680	685	
Ser Val Leu Gly Tyr Gln Gln Gly Phe Val Ile His Phe Phe Glu Val			
690	695	700	
Pro Arg Asn Asp Thr Cys Pro Glu Leu Pro Glu Ile Pro Asn Gly Trp			
705	710	715	720
Lys Ser Pro Ser Gln Pro Glu Leu Val His Gly Thr Val Val Thr Tyr			
725	730	735	
Gln Cys Tyr Pro Gly Tyr Gln Val Val Gly Ser Ser Val Leu Met Cys			
740	745	750	
Gln Trp Asp Leu Thr Trp Ser Glu Asp Leu Pro Ser Cys Gln Arg Val			
755	760	765	
Thr Ser Cys His Asp Pro Gly Asp Val Glu His Ser Arg Arg Leu Ile			
770	775	780	
Ser Ser Pro Lys Phe Pro Val Gly Ala Thr Val Gln Tyr Ile Cys Asp			
785	790	795	800
Gln Gly Phe Val Leu Thr Gly Ser Ser Ile Leu Thr Cys His Asp Arg			
805	810	815	
Gln Ala Gly Ser Pro Lys Trp Ser Asp Arg Ala Pro Lys Cys Leu Leu			
820	825	830	

Glu Gln Leu Lys Pro Cys His Gly Leu Ser Ala Pro Glu Asn Gly Ala
835 840 845

Arg Ser Pro Glu Lys Gln Leu His Pro Ala Gly Ala Thr Ile His Phe
850 855 860

Ser Cys Ala Pro Gly Tyr Val Leu Lys Gly Gln Ala Ser Ile Lys Cys
865 870 875 880

Val Pro Gly His Pro Ser His Trp Ser Asp Pro Pro Pro Ile Cys Arg
885 890 895

Ala Ala Ser Leu Asp Gly Phe Tyr Asn Ser Arg Ser Leu Asp Val Ala
900 905 910

Lys Ala Pro Ala Ala Ser Ser Thr Leu Asp Ala Ala His Ile Ala Ala
915 920 925

Ala Ile Phe Leu Pro Leu Val Ala Met Val Leu Leu Val Gly Gly Val
930 935 940

Tyr Phe Tyr Phe Ser Arg Leu Gln Gly Lys Ser Ser Leu Gln Leu Pro
945 950 955 960

Arg Pro Arg Pro Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe
965 970 975

Asp Asn Pro Thr Tyr Glu Thr Gly Ser Leu Ser Phe Ala Gly Asp Glu
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Arg Ile

<210> 17

<211> 2127

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (178)..(1752)

<220>

<223> n 2077 can be A, G, C, or T.

<400> 17

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caagcccccc gccctccgc cgcggtccca gccaggggcg cggccgcaac cagcacc 177

atg cgc ccg gta gcc ctg ctg ctc ctg ccc tcg ctg ctg gcg ctc ctg 225
 Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu
 1 5 10 15

gct cac gga ctc tct tta gag gcc cca acc gtg ggg aaa gga caa gcc 273
 Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala
 20 25 30

cca ggc atc gag gag aca gat ggc gag ctg aca gca gcc ccc aca cct 321
 Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro
 35 40 45

gag cag cca gaa cga ggc gtc cac ttt gtc aca aca gcc ccc acc ttg 369
 Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu
 50 55 60

aag ctg ctc aac cac cac ccg ctg ctt gag gaa ttc cta caa gag ggg 417
 Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly
 65 70 75 80

ctg gaa aag gga gat gag gag ctg agg cca gca ctg ccc ttc cag cct 465
 Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro
 85 90 95

gac cca cct gca ccc ttc acc cca agt ccc ctt ccc cgc ctg gcc aac 513
 Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn
 100 105 110

cag gac agc cgc cct gtc ttt acc agc ccc act cca gcc atg gct gcg 561
 Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala
 115 120 125

gta ccc act cag ccc cag tcc aag gag gga ccc tgg agt ccg gag tca 609
 Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser
 130 135 140

gag tcc cct atg ctt cga atc aca gct ccc cta cct cca ggg ccc agc 657
 Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser
 145 150 155 160

atg gca gtg ccc acc cta ggc cca ggg gag ata gcc agc act aca ccc 705
 Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro
 165 170 175

ccc agc aga gcc tgg aca cca acc caa gag ggt cct gga gac atg gga 753
 Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly
 180 185 190

agg ccg tgg gtt gca gag gtt gtg tcc cag ggc gca ggg atc ggg atc 801
 Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile
 195 200 205

cag ggg acc atc acc tcc tcc aca gct tca gga gat gat gag gag acc 849
Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr
210 215 220

acc act acc acc acc atc atc acc acc acc atc acc aca gtc cag aca 897
Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr
225 230 235 240

cca ggc cct tgt agc tgg aat ttc tca ggc cca gag ggc tct ctg gac 945
Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp
245 250 255

tcc cct aca gac ctc agc tcc ccc act gat gtt ggc ctg gac tgc ttc 993
Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe
260 265 270

ttc tac atc tct gtc tac cct ggc tat ggc gtg gaa atc aag gtc cag 1041
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln
275 280 285

aat atc agc ctc cgg gaa ggg gag aca gtg act gtg gaa ggc ctg ggg 1089
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly
290 295 300

ggg cct gac cca ctg ccc ctg gcc aac cag tct ttc ctg ctg cgg ggc 1137
Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly
305 310 315 320

caa gtc atc cgc agc ccc acc cac caa gcg gcc ctg agg ttc cag agc 1185
Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser
325 330 335

ctc ccg cca ccg gct ggc cct ggc acc ttc cat ttc cat tac caa gcc 1233
Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala
340 345 350

tat ctc ctg agc tgc cac ttt ccc cgt cgt cca gct tat gga gat gtg 1281
Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Pro Ala Tyr Gly Asp Val
355 360 365

act gtc acc agc ctc cac cca ggg ggt agt gcc cgc ttc cat tgt gcc 1329
Thr Val Thr Ser Leu His Pro Gly Gly Ser Ala Arg Phe His Cys Ala
370 375 380

act ggc tac cag ctg aag ggc gcc agg cat ctc acc tgt ctc aat gcc 1377
Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala
385 390 395 400

acc cag ccc ttc tgg gat tca aag gag ccc gtc tgc atc gct gct tgc 1425
Thr Gln Pro Phe Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys
405 410 415

ggc gga gtg atc cgc aat ggc acc acc ggc cgc atc gtc tct cca ggc 1473

Gly Gly Val Ile Arg Asn Gly Thr Thr Gly Arg Ile Val Ser Pro Gly
420 425 430

ttc ccg ggc aac tac agc aac aac ctc acc tgt cac tgg ctg ctt gag 1521
Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu
435 440 445

gct cct gag ggc cag cgg cta cac ctg cac ttt gag aag gtt tcc ctg 1569
Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu
450 455 460

gca gag gat gat gac agg ctc atc att cgc aat ggg gac aac gtg gag 1617
Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu
465 470 475 480

gcc cca cca gtg gga aaa agc tcc ctg cag ctg ccc cgc ccc cgc ccc 1665
Ala Pro Pro Val Gly Lys Ser Ser Leu Gln Leu Pro Arg Pro Arg Pro
485 490 495

cgc ccc tac aac cgc att acc ata gag tca gcg ttt gac aat cca act 1713
Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe Asp Asn Pro Thr
500 505 510

tac gag act gga gag acg aga gaa tat gaa gtc tcc atc taggtggggg 1762
Tyr Glu Thr Gly Glu Thr Arg Glu Tyr Glu Val Ser Ile
515 520 525

cagtctaggg aagtcaactc agacttcac cacagtccag cagcaaggct ccttgcttcc 1822

tgctgtccct ccacctctg tatataccac ctaggaggag atgccaccaa gccctcaaga 1882

agttgtgccc tccccgcct gcgatgccca ccatggccta tttcttggt gtcattgccc 1942

acttggggcc cttgcattgg gccatgtaca gggggcatct acctgtgggg aagaacatag 2002

ctgggagcac aagcttcaac agccagcatt ccttgagcct cttcatggc cctgggacca 2062

gcctggggaa cacanttagg caggagcagg gagttacctt gtttcacatg accaccaacc 2122

attcc 2127

<210> 18

<211> 525

<212> PRT

<213> Homo sapiens

<223> n 2077 can be A, G, C, or T.

<400> 18

Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu

1 5 10 15

Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala

20	25	30
Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro		
35	40	45
Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu		
50	55	60
Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly		
65	70	75
80		
Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro		
85	90	95
Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn		
100	105	110
Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala		
115	120	125
Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser		
130	135	140
Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser		
145	150	155
160		
Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro		
165	170	175
Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly		
180	185	190
Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile		
195	200	205
Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr		
210	215	220
Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr		
225	230	235
240		
Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp		
245	250	255
Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe		
260	265	270
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln		
275	280	285
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly		
290	295	300

Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly
305 310 315 320

Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser
325 330 335

Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala
340 345 350

Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Pro Ala Tyr Gly Asp Val
355 360 365

Thr Val Thr Ser Leu His Pro Gly Gly Ser Ala Arg Phe His Cys Ala
370 375 380

Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala
385 390 395 400

Thr Gln Pro Phe Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys
405 410 415

Gly Gly Val Ile Arg Asn Gly Thr Thr Gly Arg Ile Val Ser Pro Gly
420 425 430

Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu
435 440 445

Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu
450 455 460

Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu
465 470 475 480

Ala Pro Pro Val Gly Lys Ser Ser Leu Gln Leu Pro Arg Pro Arg Pro
485 490 495

Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe Asp Asn Pro Thr
500 505 510

Tyr Glu Thr Gly Glu Thr Arg Glu Tyr Glu Val Ser Ile
515 520 525

<210> 19

<211> 2127

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (178)..(1752)

<220>

<223> n 2077 can be A, G, C, or T.

<400> 19

ccaggcgctg gccgtggtgc tgattctgtc aggcgctggc ggccgcagcg gcggtgacgg 60

ctgcggcccc gtcctctcta cccggccgga cccggtcttg cccccgcgcc caagccccac 120

caagcccccc gccctcccg cgcgggtccca gcccagggcg cggccgcaac cagcacc 177

atg cgc ccg gta gcc ctg ctg ctc ctg ccc tcg ctg ctg gcg ctc ctg 225

Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu

1 5 10 15

gct cac gga ctc tct tta gag gcc cca acc gtg ggg aaa gga caa gcc 273

Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala

20 25 30

cca ggc atc gag gag aca gat ggc gag ctg aca gca gcc ccc aca cct 321

Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro

35 40 45

gag cag cca gaa cga ggc gtc cac ttt gtc aca aca gcc ccc acc ttg 369

Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu

50 55 60

aag ctg ctc aac cac cac ccg ctg ctt gag gaa ttc cta caa gag ggg 417

Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly

65 70 75 80

ctg gaa aag gga gat gag gag ctg agg cca gca ctg ccc ttc cag cct 465

Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro

85 90 95

gac cca cct gca ccc ttc acc cca agt ccc ctt ccc cgc ctg gcc aac 513

Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn

100 105 110

cag gac agc cgc cct gtc ttt acc agc ccc act cca gcc atg gct gcg 561

Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala

115 120 125

gta ccc act cag ccc cag tcc aag gag gga ccc tgg agt ccg gag tca 609

Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser

130 135 140

gag tcc cct atg ctt cga atc aca gct ccc cta cct cca ggg ccc agc 657

Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser

145 150 155 160

atg gca gtg ccc acc cta ggc cca ggg gag ata gcc agc act aca ccc 705

Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro

165 170 175

ccc agc aga gcc tgg aca cca acc caa gag ggt cct gga gac atg gga 753
Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly
180 185 190

agg ccg tgg gtt gca gag gtt gtg tcc cag ggc gca ggg atc ggg atc 801
Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile
195 200 205

cag ggg acc atc acc tcc tcc aca gct tca gga gat gat gag gag acc 849
Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr
210 215 220

acc act acc acc acc atc atc acc acc acc atc acc aca gtc cag aca 897
Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr
225 230 235 240

cca ggc cct tgt agc tgg aat ttc tca ggc cca gag ggc tct ctg gac 945
Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp
245 250 255

tcc cct aca gac ctc agc tcc ccc act gat gtt ggc ctg gac tgc ttc 993
Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe
260 265 270

ttc tac atc tct gtc tac cct ggc tat ggc gtg gaa atc aag gtc cag 1041
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln
275 280 285

aat atc agc ctc cgg gaa ggg gag aca gtg act gtg gaa ggc ctg ggg 1089
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly
290 295 300

ggg cct gac cca ctg ccc ctg gcc aac cag tct ttc ctg ctg cgg ggc 1137
Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly
305 310 315 320

caa gtc atc cgc agc ccc acc cac caa gcg gcc ctg agg ttc cag agc 1185
Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser
325 330 335

ctc ccg cca ccg gct ggc cct ggc acc ttc cat ttc cat tac caa gcc 1233
Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala
340 345 350

tat ctc ctg agc tgc cac ttt ccc cgt cgt cca gct tat gga gat gtg 1281
Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Pro Ala Tyr Gly Asp Val
355 360 365

act gtc acc agc ctc cac cca ggg ggt agt gcc cgc ttc cat tgt gcc 1329
Thr Val Thr Ser Leu His Pro Gly Ser Ala Arg Phe His Cys Ala
370 375 380

act ggc tac cag ctg aag ggc gcc agg cat ctc acc tgt ctc aat gcc 1377
 Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala
 385 390 395 400

acc cag ccc ttc tgg gat tca aag gag ccc gtc tgc atc gct gct tgc 1425
 Thr Gln Pro Phe Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys
 405 410 415

ggc gga gtg atc cgc aat ggc acc acc ggc cgc atc gtc tct cca ggc 1473
 Gly Gly Val Ile Arg Asn Gly Thr Thr Gly Arg Ile Val Ser Pro Gly
 420 425 430

ttc ccg ggc aac tac agc aac aac ctc acc tgt cac tgg ctg ctt gag 1521
 Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu
 435 440 445

gct cct gag ggc cag cgg cta cac ctg cac ttt gag aag gtt tcc ctg 1569
 Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu
 450 455 460

gca gag gat gat gac agg ctc atc att cgc aat ggg gac aac gtg gag 1617
 Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu
 465 470 475 480

gcc cca cca gtg tat gat tcc tat gag gtg gaa tac ccg ccc cgc ccc 1665
 Ala Pro Pro Val Tyr Asp Ser Tyr Glu Val Glu Tyr Pro Pro Arg Pro
 485 490 495

cgc ccc tac aac cgc att acc ata gag tca gcg ttt gac aat cca act 1713
 Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe Asp Asn Pro Thr
 500 505 510

tac gag act gga gag acg aga gaa tat gaa gtc tcc atc taggtggggg 1762
 Tyr Glu Thr Gly Glu Thr Arg Glu Tyr Glu Val Ser Ile
 515 520 525

cagtctaggg aagtcaactc agacttcac cacagtccag cagcaaggct ccttgcttcc 1822

tgctgtccct ccacctctg tatataccac ctaggaggag atgccaccaa gccctcaaga 1882

agttgtgccc ttccccgcct gcgatgccca ccatggccta ttttcttggg gtcattgccc 1942

acttggggcc ctgcatgg gccatgtaca gggggcatct acctgtgggg aagaacatag 2002

ctgggagcac aagcttcaac agccagcatt ccttgagcct ccttcatggc cctgggacca 2062

gcctggggaa cacanttagg caggagcagg gagttacctt gttcacatg accaccaacc 2122

attcc

2127

<210> 20

<211> 525

<212> PRT

<213> Homo sapiens

<223> n 2077 can be A, G, C, or T.

<400> 20

Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu
1 5 10 15

Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala
20 25 30

Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro
35 40 45

Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu
50 55 60

Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly
65 70 75 80

Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro
85 90 95

Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn
100 105 110

Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala
115 120 125

Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser
130 135 140

Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser
145 150 155 160

Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro
165 170 175

Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly
180 185 190

Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile
195 200 205

Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr
210 215 220

Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr
225 230 235 240

Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp
245 250 255

Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe
260 265 270

Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln
275 280 285

Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly
290 295 300

Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly
305 310 315 320

Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser
325 330 335

Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala
340 345 350

Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Pro Ala Tyr Gly Asp Val
355 360 365

Thr Val Thr Ser Leu His Pro Gly Gly Ser Ala Arg Phe His Cys Ala
370 375 380

Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala
385 390 395 400

Thr Gln Pro Phe Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys
405 410 415

Gly Gly Val Ile Arg Asn Gly Thr Thr Gly Arg Ile Val Ser Pro Gly
420 425 430

Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu
435 440 445

Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu
450 455 460

Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu
465 470 475 480

Ala Pro Pro Val Tyr Asp Ser Tyr Glu Val Glu Tyr Pro Pro Arg Pro
485 490 495

Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe Asp Asn Pro Thr
500 505 510

Tyr Glu Thr Gly Glu Thr Arg Glu Tyr Glu Val Ser Ile
515 520 525

<210> 21
<211> 1988
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (178)..(1752)

<400> 21
ccaggcgctg gccgtggtgc tgattctgtc aggcgctggc ggcggcagcg gcggtgacgg 60

ctgcggcccc gctccctcta cccggccgga cccggctctg cccccgcgcc caagccccac 120

caagcccccc gccctccgc cgcggtccca gcccaggcg cggccgaac cagcacc 177

atg cgc ccg gta gcc ctg ctg ctc ctg ccc tcg ctg ctg gcg ctc ctg 225
Met Arg Pro Val Ala Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu
1 5 10 15

gct cac gga ctc tct tta gag gcc cca acc gtg ggg aaa gga caa gcc 273
Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala
20 25 30

cca ggc atc gag gag aca gat ggc gag ctg aca gca gcc ccc aca cct 321
Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro
35 40 45

gag cag cca gaa cga ggc gtc cac ttt gtc aca aca gcc ccc acc ttg 369
Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu
50 55 60

aag ctg ctc aac cac cac ccg ctg ctt gag gaa ttc cta caa gag ggg 417
Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly
65 70 75 80

ctg gaa aag gga gat gag gag ctg agg cca gca ctg ccc ttc cag cct 465
Leu Glu Lys Gly Asp Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro
85 90 95

gac cca cct gca ccc ttc acc cca agt ccc ctt ccc cgc ctg gcc aac 513
Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn
100 105 110

cag gac agc cgc cct gtc ttt acc agc ccc act cca gcc atg gct gcg 561
Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala
115 120 125

gta ccc act cag ccc cag tcc aag gag gga ccc tgg agt ccg gag tca 609
Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser
130 135 140

gag tcc cct atg ctt cga atc aca gct ccc cta cct cca ggg ccc agc 657

Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser
145 150 155 160

atg gca gtg ccc acc cta ggc cca ggg gag ata gcc agc act aca ccc 705
Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro
 165 170 175

ccc agc aga gcc tgg aca cca acc caa gag ggt cct gga gac atg gga 753
Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly
 180 185 190

agg ccg tgg gtt gca gag gtt gtg tcc cag ggc gca ggg atc ggg atc 801
Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile
 195 200 205

cag ggg acc atc acc tcc tcc aca gct tca gga gat gat gag gag acc 849
Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr
 210 215 220

acc act acc acc acc atc atc acc acc acc atc acc aca gtc cag aca 897
Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr
225 230 235 240

cca ggc cct tgt agc tgg aat ttc tca ggc cca gag ggc tct ctg gac 945
Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp
 245 250 255

tcc cct aca gac ctg agc tcc ccc act gat gtt ggc ctg gac tgc ttc 993
Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe
 260 265 270

ttc tac atc tct gtc tac cct ggc tat ggc gtg gaa atc aag gtc cag 1041
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln
 275 280 285

aat atc agc ctg cgg gaa ggg gag aca gtg act gtg gaa ggc ctg ggg 1089
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly
 290 295 300

ggg cct gac cca ctg ccc ctg gcc aac cag tct ttc ctg ctg cgg ggc 1137
Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly
305 310 315 320

caa gtc atc cgc agc ccc acc cac caa gcg gcc ctg agg ttc cag agc 1185
Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser
 325 330 335

ctc ccg cca ccg gct ggc cct ggc acc ttc cat ttc cat tac caa gcc 1233
Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala
 340 345 350

tat ctg ctg agc tgc cac ttt ccc cgt cgt cca gct tat gga gat gtg 1281
Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Pro Ala Tyr Gly Asp Val

355	360	365	
act gtc acc agc ctc cac cca ggg ggt agt gcc cgc ttc cat tgt gcc 1329			
Thr Val Thr Ser Leu His Pro Gly Gly Ser Ala Arg Phe His Cys Ala			
370	375	380	
act ggc tac cag ctg aag ggc gcc agg cat ctc acc tgt ctc aat gcc 1377			
Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala			
385	390	395	400
acc cag ccc ttc tgg gat tca aag gag ccc gtc tgc atc gct gct tgc 1425			
Thr Gln Pro Phe Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys			
405	410	415	
ggc gga gtg atc cgc aat ggc acc acc ggc cgc atc gtc tct cca ggc 1473			
Gly Gly Val Ile Arg Asn Gly Thr Thr Gly Arg Ile Val Ser Pro Gly			
420	425	430	
ttc ccg ggc aac tac agc aac aac ctc acc tgt cac tgg ctg ctt gag 1521			
Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu			
435	440	445	
gct cct gag ggc cag cgg cta cac ctg cac ttt gag aag gtt tcc ctg 1569			
Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu			
450	455	460	
gca gag gat gat gac agg ctc atc att cgc aat ggg gac aac gtg gag 1617			
Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu			
465	470	475	480
gcc cca cca gtg tat gat tcc tat gag gtg gaa tac ccg ccc cgc ccc 1665			
Ala Pro Pro Val Tyr Asp Ser Tyr Glu Val Glu Tyr Pro Pro Arg Pro			
485	490	495	
cgc ccc tac aac cgc att acc ata gag tca gcg ttt gac aat cca act 1713			
Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe Asp Asn Pro Thr			
500	505	510	
tac gag act gga gag acg aga gaa tat gaa gtc tcc atc taggtggggg 1762			
Tyr Glu Thr Gly Glu Thr Arg Glu Tyr Glu Val Ser Ile			
515	520	525	
cagtctaggg aagtcaactc agacttgcac cacagtccag cagcaaggct ccttgcttcc 1822			
tgctgtccct ccacctctg tatataccac ctaggaggag atgccaccaa gccactttgt 1882			
acatgtaatg tattatatgg ggtctgggct ccagccagag aacaatcttt tatttctgtt 1942			
gtttccttat taaatggtg ttttgaaa aaaaaaaaaa aaaaaa 1988			

<210> 22
<211> 525

<212> PRT

<213> Homo sapiens

<400> 22

Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu
1 5 10 15

Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala
20 25 30

Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro
35 40 45

Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu
50 55 60

Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly
65 70 75 80

Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro
85 90 95

Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn
100 105 110

Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala
115 120 125

Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser
130 135 140

Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser
145 150 155 160

Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro
165 170 175

Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly
180 185 190

Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile
195 200 205

Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr
210 215 220

Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr
225 230 235 240

Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp
245 250 255

Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe

260	265	270
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln		
275	280	285
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly		
290	295	300
Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly		
305	310	315 320
Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser		
325	330	335
Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala		
340	345	350
Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Pro Ala Tyr Gly Asp Val		
355	360	365
Thr Val Thr Ser Leu His Pro Gly Gly Ser Ala Arg Phe His Cys Ala		
370	375	380
Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala		
385	390	395 400
Thr Gln Pro Phe Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys		
405	410	415
Gly Gly Val Ile Arg Asn Gly Thr Thr Gly Arg Ile Val Ser Pro Gly		
420	425	430
Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu		
435	440	445
Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu		
450	455	460
Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu		
465	470	475 480
Ala Pro Pro Val Tyr Asp Ser Tyr Glu Val Glu Tyr Pro Pro Arg Pro		
485	490	495
Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe Asp Asn Pro Thr		
500	505	510
Tyr Glu Thr Gly Glu Thr Arg Glu Tyr Glu Val Ser Ile		
515	520	525

<210> 23

<211> 2143
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (178)..(1755)

<220>
<223> n 2093 can be A, G, C, or T.

<400> 23
ccaggcgctg gccgtggtgc tgattctgtc aggcgctggc ggcggcagcg gcggtgacgg 60
ctgcggcccc gctccctcta cccggccgga cccggctctg cccccgcgcc caagccccac 120
caagcccccc gccctccgcg cgcggtcca gccagggcg cgccgcaac cagcacc 177

atg cgc ccg gta gcc ctg ctg ctc ctg ccc tcg ctg ctg gcg ctc ctg 225
Met Arg Pro Val Ala Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu
1 5 10 15

gct cac gga ctc tct tta gag gcc cca acc gtg ggg aaa gga caa gcc 273
Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala
20 25 30

cca ggc atc gag gag aca gat ggc gag ctg aca gca gcc ccc aca cct 321
Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro
35 40 45

gag cag cca gaa cga ggc gtc cac ttt gtc aca aca gcc ccc acc ttg 369
Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu
50 55 60

aag ctg ctc aac cac cac ccg ctg ctt gag gaa ttc cta caa gag ggg 417
Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly
65 70 75 80

ctg gaa aag gga gat gag gag ctg agg cca gca ctg ccc ttc cag cct 465
Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro
85 90 95

gac cca cct gca ccc ttc acc cca agt ccc ctt ccc cgc ctg gcc aac 513
Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn
100 105 110

cag gac agc cgc cct gtc ttt acc agc ccc act cca gcc atg gct gcg 561
Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala
115 120 125

gta ccc act cag ccc cag tcc aag gag gga ccc tgg agt ccg gag tca 609
Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser
130 135 140

gag tcc cct atg ctt cga atc aca gct ccc cta cct cca ggg ccc agc 657
Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser
145 150 155 160

atg gca gtg ccc acc cta ggc cca ggg gag ata gcc agc act aca ccc 705
Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro
165 170 175

ccc agc aga gcc tgg aca cca acc caa gag ggt cct gga gac atg gga 753
Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly
180 185 190

agg ccg tgg gtt gca gag gtt gtg tcc cag ggc gca ggg atc ggg atc 801
Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile
195 200 205

cag ggg acc atc acc tcc tcc aca gct tca gga gat gat gag gag acc 849
Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr
210 215 220

acc act acc acc acc atc atc acc acc acc atc acc aca gtc cag aca 897
Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr
225 230 235 240

cca ggc cct tgt agc tgg aat ttc tca ggc cca gag ggc tct ctg gac 945
Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp
245 250 255

tcc cct aca gac ctc agc tcc ccc act gat gtt ggc ctg gac tgc ttc 993
Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe
260 265 270

ttc tac atc tct gtc tac cct ggc tat ggc gtg gaa atc aag gtc cag 1041
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln
275 280 285

aat atc agc ctc cgg gaa ggg gag aca gtg act gtg gaa ggc ctg ggg 1089
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly
290 295 300

ggg cct gac cca ctg ccc ctg gcc aac cag tct ttc ctg ctg cgg ggc 1137
Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly
305 310 315 320

caa gtc atc cgc agc ccc acc cac caa gcg gcc ctg agg ttc cag agc 1185
Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser
325 330 335

ctc ccg cca ccg gct ggc cct ggc acc ttc cat ttc cat tac caa gcc 1233
Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala
340 345 350

tat ctc ctg agc tgc cac ttt ccc cgt cgt cca gct tat gga gat gtg 1281
Tyr Leu Ser Cys His Phe Pro Arg Arg Pro Ala Tyr Gly Asp Val
355 360 365

act gtc acc agc ctc cac cca ggg ggt agt gcc cgc ttc cat tgt gcc 1329
Thr Val Thr Ser Leu His Pro Gly Gly Ser Ala Arg Phe His Cys Ala
370 375 380

act ggc tac cag ctg aag ggc gcc agg cat ctc acc tgt ctc aat gcc 1377
Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala
385 390 395 400

acc cag ccc ttc tgg gat tca aag gag ccc gtc tgc atc gct gct tgc 1425
Thr Gln Pro Phe Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys
405 410 415

ggc gga gtg atc cgc aat ggc acc acc ggc cgc atc gtc tct cca ggc 1473
Gly Gly Val Ile Arg Asn Gly Thr Thr Gly Arg Ile Val Ser Pro Gly
420 425 430

ttc ccg ggc aac tac agc aac aac ctc acc tgt cac tgg ctg ctt gag 1521
Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu
435 440 445

gct cct gag ggc cag cgg cta cac ctg cac ttt gag aag gtt tcc ctg 1569
Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu
450 455 460

gca gag gat gat gac agg ctc atc att cgc aat ggg gac aac gtg gag 1617
Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu
465 470 475 480

gcc cca cca gtg gga aaa agc tcc ctg cag ctg ccc cgc ccc cgc ccc 1665
Ala Pro Pro Val Gly Lys Ser Ser Leu Gln Leu Pro Arg Pro Arg Pro
485 490 495

cgc ccc tac aac cgc att acc ata gag tca gcg ttt gac aat cca act 1713
Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe Asp Asn Pro Thr
500 505 510

tac gag act gga tct ctt tcc ttt gca gga gac gag aga ata 1755
Tyr Glu Thr Gly Ser Leu Ser Phe Ala Gly Asp Glu Arg Ile
515 520 525

tgaagtctcc atctaggtgg gggcagtcta gggaagtcaa ctgagacttg caccacagtc 1815

cagcagcaag gctccttgct tctgctgtc cctccacctc ctgtatatac cacctaggag 1875

gagatgccac caagccctca agaagttgtg cccttccccg cctgcgatgc ccaccatggc 1935

ctattttctt ggtgtcattg cccacttggg gcccttgcat tgggcatgt acagggggca 1995

tctacctgtg gggaagaaca tagctgggag cacaagcttc aacagccagc attccttgag 2055

cctccttcat ggccctggga ccagcctggg gaacacantt aggcaggagc agggagttac 2115

cttgtttcac atgaccacca accattcc 2143

<210> 24

<211> 526

<212> PRT

<213> Homo sapiens

<223> n 2093 can be A, G, C, or T.

<400> 24

Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu

1 5 10 15

Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala

20 25 30

Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro

35 40 45

Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu

50 55 60

Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly

65 70 75 80

Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro

85 90 95

Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn

100 105 110

Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala

115 120 125

Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser

130 135 140

Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser

145 150 155 160

Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro

165 170 175

Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly

180 185 190

Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile

195 200 205

Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr

210	215	220
Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr		
225	230	235 240
Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp		
245	250	255
Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe		
260	265	270
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln		
275	280	285
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly		
290	295	300
Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly		
305	310	315 320
Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser		
325	330	335
Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala		
340	345	350
Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Pro Ala Tyr Gly Asp Val		
355	360	365
Thr Val Thr Ser Leu His Pro Gly Gly Ser Ala Arg Phe His Cys Ala		
370	375	380
Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala		
385	390	395 400
Thr Gln Pro Phe Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys		
405	410	415
Gly Gly Val Ile Arg Asn Gly Thr Thr Gly Arg Ile Val Ser Pro Gly		
420	425	430
Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu		
435	440	445
Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu		
450	455	460
Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu		
465	470	475 480
Ala Pro Pro Val Gly Lys Ser Ser Leu Gln Leu Pro Arg Pro Arg Pro		
485	490	495

Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe Asp Asn Pro Thr
500 505 510

Tyr Glu Thr Gly Ser Leu Ser Phe Ala Gly Asp Glu Arg Ile
515 520 525

<210> 25
<211> 1482
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (178)..(960)

<400> 25
ccaggcgctg gccgtggtgc tgattctgtc aggcgctggc ggccgcagcg gcggtgacgg 60
ctgcggcccc gctccctcta cccggccgga cccggctctg ccccgcgcc caagccccac 120
caagcccccc gccctccgc cgcggtccca gcccagggcg cggccgcaac cagcacc 177

atg cgc ccg gta gcc ctg ctg ctc ctg ccc tcg ctg ctg gcg ctc ctg 225
Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu
1 5 10 15

gct cac gga ctc tct tta gag gcc cca acc gtg ggg aaa gga caa gcc 273
Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala
20 25 30

cca ggc atc gag gag aca gat ggc gag ctg aca gca gcc ccc aca cct 321
Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro
35 40 45

gag cag cca gaa cga ggc gtc cac ttt gtc aca aca gcc ccc acc ttg 369
Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu
50 55 60

aag ctg ctc aac cac cac ccg ctg ctt gag gaa ttc cta caa gag ggg 417
Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly
65 70 75 80

ctg gaa aag gga gat gag gag ctg agg cca gca ctg ccc ttc cag cct 465
Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro
85 90 95

gac cca cct gca ccc ttc acc cca agt ccc ctt ccc cgc ctg gcc aac 513
Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn
100 105 110

cag gac agc cgc cct gtc ttt acc agc ccc act cca gcc atg gct gcg 561

Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala
115 120 125

gta ccc act cag ccc cag tcc aag gag gga ccc tgg agt ccg gag tca 609
Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser
130 135 140

gag tcc cct atg ctt cga atc aca gct ccc cta cct cca ggg ccc agc 657
Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser
145 150 155 160

atg gca gtg ccc acc cta ggc cca ggg gag ata gcc agc act aca ccc 705
Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro
165 170 175

ccc agc aga gcc tgg aca cca acc caa gag ggt cct gga gac atg gga 753
Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly
180 185 190

agg ccg tgg gtt gca gag gtt gtg tcc cag ggc gca ggg atc ggg atc 801
Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile
195 200 205

cag ggg acc atc acc tcc tcc aca gct tca gga gat gat gag gag acc 849
Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr
210 215 220

acc act acc acc acc atc atc acc acc acc atc acc aca gtc cag aca 897
Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr
225 230 235 240

cca ggt cag cta cct gct ggc ttg cag atg tgg aaa tgg gga tgg ggg 945
Pro Gly Gln Leu Pro Ala Gly Leu Gln Met Trp Lys Trp Gly Trp Gly
245 250 255

agg ctg cgg ggc ccc taaaagcctg tctctgacac tgtgccagcc tgcctgccc 1000
Arg Leu Arg Gly Pro
260

tttggcacca agggccagcc tgcaggaggc atgtagattg gacccagata gacctgagct 1060

caaatcctga ttcttcagcc aagtacagtg gctcatgcct gtaatccag cactttggga 1120

ggcagaggcc agtggatcat ctgaggctcag gaggtaaga ccctcctggc caacatggcg 1180

aaacaccatc tctactaaaa atacaaaaat gagccgggca tgggtggtggg cacctgtaat 1240

cccagctact cgggaggctg aggcaggaga atcactcaaa cctgggaggc agagggttga 1300

gtgagctgag attgcacat tgactccag cctgggcaac agagcgagac tctgtctcaa 1360

aaaagaaaa atcttgattc ttcaactat aacatgacc taggaattct atttaacatc 1420

tcattctga gcctcatctg taaaatggca ataagaaaat aaacttctgg ctagaaaaaa 1480

aa

1482

<210> 26

<211> 261

<212> PRT

<213> Homo sapiens

<400> 26

Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu

1 5 10 15

Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala

20 25 30

Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro

35 40 45

Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu

50 55 60

Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly

65 70 75 80

Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro

85 90 95

Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn

100 105 110

Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala

115 120 125

Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser

130 135 140

Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser

145 150 155 160

Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro

165 170 175

Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly

180 185 190

Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile

195 200 205

Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr

210 215 220

Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr
225 230 235 240

Pro Gly Gln Leu Pro Ala Gly Leu Gln Met Trp Lys Trp Gly Trp Gly
245 250 255

Arg Leu Arg Gly Pro
260

<210> 27
<211> 3336
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (120)..(2639)

<220>
<223> n 3325 can be A, G, C, or T.

<400> 27
cgccggtggc tcggcggcgg cgccggcggc ggccggcggc gggcggcggc cgctcgtctac 60

ctccagctcc tctcctcc tctcctct cctcctct ctctcatct gctgtggtt 119

atg gcc tgt cgc tgg agc aca aaa gag tct ccg cgg tgg agg tct gcg 167
Met Ala Cys Arg Trp Ser Thr Lys Glu Ser Pro Arg Trp Arg Ser Ala
1 5 10 15

tgt ctc ttg ctt ttc ctc gct ggg gtg tac gct tgt gga gag act cca 215
Leu Leu Leu Leu Phe Leu Ala Gly Val Tyr Ala Cys Gly Glu Thr Pro
20 25 30

gag caa ata cga gca cca agt ggc ata atc aca agc cca ggc tgg cct 263
Glu Gln Ile Arg Ala Pro Ser Gly Ile Ile Thr Ser Pro Gly Trp Pro
35 40 45

tct gaa tat cct gca aaa atc aac tgt agc tgg ttc ata agg gca aac 311
Ser Glu Tyr Pro Ala Lys Ile Asn Cys Ser Trp Phe Ile Arg Ala Asn
50 55 60

cca ggc gaa atc att act ata agt ttt cag gat ttt gat att caa gga 359
Pro Gly Glu Ile Ile Thr Ile Ser Phe Gln Asp Phe Asp Ile Gln Gly
65 70 75 80

tcc aga agg tgc aat ttg gac tgg ttg aca ata gaa aca tac aag aat 407
Ser Arg Arg Cys Asn Leu Asp Trp Leu Thr Ile Glu Thr Tyr Lys Asn
85 90 95

att gaa agt tac aga gct tgt ggt tcc aca att cca cct ccg tat atc 455

Ile Glu Ser Tyr Arg Ala Cys Gly Ser Thr Ile Pro Pro Pro Tyr Ile
100 105 110

tct tca caa gac cac atc tgg att agg ttt cat tcg gat gac aac atc 503
Ser Ser Gln Asp His Ile Trp Ile Arg Phe His Ser Asp Asp Asn Ile
115 120 125

tct aga aag ggt ttc aga ctg gca tat ttt tca ggg aaa tct gag gaa 551
Ser Arg Lys Gly Phe Arg Leu Ala Tyr Phe Ser Gly Lys Ser Glu Glu
130 135 140

cca aat tgt gct tgt gat cag ttt cgt tgt ggt aat gga aag tgt ata 599
Pro Asn Cys Ala Cys Asp Gln Phe Arg Cys Gly Asn Gly Lys Cys Ile
145 150 155 160

cca gaa gcc tgg aaa tgc aat aac atg gat gaa tgt gga gat agt tcc 647
Pro Glu Ala Trp Lys Cys Asn Asn Met Asp Glu Cys Gly Asp Ser Ser
165 170 175

gat gaa gag atc tgt gcc aaa gaa gca aat cct cca act gct gct gct 695
Asp Glu Glu Ile Cys Ala Lys Glu Ala Asn Pro Pro Thr Ala Ala Ala
180 185 190

ttt caa ccc tgt gct tac aac cag ttc cag tgt tta tcc cgt ttt acc 743
Phe Gln Pro Cys Ala Tyr Asn Gln Phe Gln Cys Leu Ser Arg Phe Thr
195 200 205

aaa gtt tac act tgc ctc ccc gaa tct tta aaa tgt gat ggg aac att 791
Lys Val Tyr Thr Cys Leu Pro Glu Ser Leu Lys Cys Asp Gly Asn Ile
210 215 220

gac tgc ctt gac cta gga gat gag ata gac tgt gat gtg cca aca tgt 839
Asp Cys Leu Asp Leu Gly Asp Glu Ile Asp Cys Asp Val Pro Thr Cys
225 230 235 240

ggg caa tgg cta aaa tat ttt tat ggt act ttt aat tct ccc aat tat 887
Gly Gln Trp Leu Lys Tyr Phe Tyr Gly Thr Phe Asn Ser Pro Asn Tyr
245 250 255

cca gac ttt tat cct cct gga agc aat tgc acc tgg tta ata gac act 935
Pro Asp Phe Tyr Pro Pro Gly Ser Asn Cys Thr Trp Leu Ile Asp Thr
260 265 270

ggt gat cac cgt aaa gtc att tta cgc ttc act gac ttt aaa ctt gat 983
Gly Asp His Arg Lys Val Ile Leu Arg Phe Thr Asp Phe Lys Leu Asp
275 280 285

ggt act ggt tat ggt gat tat gtc aaa ata tat gat gga tta gag gag 1031
Gly Thr Gly Tyr Gly Asp Tyr Val Lys Ile Tyr Asp Gly Leu Glu Glu
290 295 300

aat cca cac aag ctt ttg cgt gtg ttg aca gct ttt gat tct cat gca 1079
Asn Pro His Lys Leu Leu Arg Val Leu Thr Ala Phe Asp Ser His Ala

305	310	315	320
cct ctt aca gtt gtt tct tct tct gga cag ata agg gta cat ttt tgt 1127			
Pro Leu Thr Val Val Ser Ser Ser Gly Gln Ile Arg Val His Phe Cys			
325	330	335	
gct gat aaa gtg aat gct gca agg gga ttt aat gct act tac caa gta 1175			
Ala Asp Lys Val Asn Ala Ala Arg Gly Phe Asn Ala Thr Tyr Gln Val			
340	345	350	
gat ggg ttc tgt ttg cca tgg gaa ata ccc tgt gga ggt aac tgg ggg 1223			
Asp Gly Phe Cys Leu Pro Trp Glu Ile Pro Cys Gly Gly Asn Trp Gly			
355	360	365	
tgt tat act gag cag cag cgt tgt gat ggg tat tgg cat tgc cca aat 1271			
Cys Tyr Thr Glu Gln Gln Arg Cys Asp Gly Tyr Trp His Cys Pro Asn			
370	375	380	
gga agg gat gaa acc aat tgt acc atg tgc cag aag gaa gaa ttt cca 1319			
Gly Arg Asp Glu Thr Asn Cys Thr Met Cys Gln Lys Glu Glu Phe Pro			
385	390	395	400
tgt tcc cga aat ggt gtc tgt tat cct cgt tct gat cgc tgc aac tac 1367			
Cys Ser Arg Asn Gly Val Cys Tyr Pro Arg Ser Asp Arg Cys Asn Tyr			
405	410	415	
cag aat cat tgc cca aat ggc tca gat gaa aaa aac tgc ttt ttt tgc 1415			
Gln Asn His Cys Pro Asn Gly Ser Asp Glu Lys Asn Cys Phe Phe Cys			
420	425	430	
caa cca gga aat ttc cat tgt aaa aac aat cgt tgt gtg ttt gaa agt 1463			
Gln Pro Gly Asn Phe His Cys Lys Asn Asn Arg Cys Val Phe Glu Ser			
435	440	445	
tgg gtg tgt gat tct caa gat gac tgt ggt gat ggc agc gat gaa gaa 1511			
Trp Val Cys Asp Ser Gln Asp Asp Cys Gly Asp Gly Ser Asp Glu Glu			
450	455	460	
aat tgc cca gta atc gtg cct aca aga gtc atc act gct gcc gtc ata 1559			
Asn Cys Pro Val Ile Val Pro Thr Arg Val Ile Thr Ala Ala Val Ile			
465	470	475	480
ggg agc ctc atc tgt ggc ctg tta ctc gtc ata gca ttg gga tgt act 1607			
Gly Ser Leu Ile Cys Gly Leu Leu Val Ile Ala Leu Gly Cys Thr			
485	490	495	
tgt aag ctt tat tct ctg aga atg ttt gaa aga aga tca ttt gaa aca 1655			
Cys Lys Leu Tyr Ser Leu Arg Met Phe Glu Arg Arg Ser Phe Glu Thr			
500	505	510	
cag ttg tca aga gtg gaa gca gaa ttg tta aga aga gaa gct cct ccc 1703			
Gln Leu Ser Arg Val Glu Ala Glu Leu Leu Arg Arg Glu Ala Pro Pro			
515	520	525	

tcg tat gga caa ttg att gct cag ggt tta att cca cca gtt gaa gat 1751
Ser Tyr Gly Gln Leu Ile Ala Gln Gly Leu Ile Pro Pro Val Glu Asp
530 535 540

ttt cct gtt tgt tca cct aat cag gct tct gtt ttg gaa aat ctg agg 1799
Phe Pro Val Cys Ser Pro Asn Gln Ala Ser Val Leu Glu Asn Leu Arg
545 550 555 560

cta gcg gta cga tct cag ctt gga ttt act tca gtc agg ctt cct atg 1847
Leu Ala Val Arg Ser Gln Leu Gly Phe Thr Ser Val Arg Leu Pro Met
565 570 575

gca ggc aga tca agc aac att tgg aac cgt att ttt aat ttt gca aga 1895
Ala Gly Arg Ser Ser Asn Ile Trp Asn Arg Ile Phe Asn Phe Ala Arg
580 585 590

tca cgt cat tct ggg tca ttg gct ttg gtc tca gca gat gga gat gag 1943
Ser Arg His Ser Gly Ser Leu Ala Leu Val Ser Ala Asp Gly Asp Glu
595 600 605

gtt gtc cct agt cag agt acc agt aga gaa cct gag aga aat cat act 1991
Val Val Pro Ser Gln Ser Thr Ser Arg Glu Pro Glu Arg Asn His Thr
610 615 620

cac aga agt ttg ttt tcc gtg gag tct gat gat aca gac aca gaa aat 2039
His Arg Ser Leu Phe Ser Val Glu Ser Asp Asp Thr Asp Thr Glu Asn
625 630 635 640

gag aga aga gat atg gca gga gca tct ggt ggg gtt gca gct cct ttg 2087
Glu Arg Arg Asp Met Ala Gly Ala Ser Gly Gly Val Ala Ala Pro Leu
645 650 655

cct caa aaa gtc cct ccc aca acg gca gta gaa gcg aca gta gga gca 2135
Pro Gln Lys Val Pro Pro Thr Thr Ala Val Glu Ala Thr Val Gly Ala
660 665 670

tgt gca agt tcc tca act cag agt acc cga ggt ggt cat gca gat aat 2183
Cys Ala Ser Ser Ser Thr Gln Ser Thr Arg Gly Gly His Ala Asp Asn
675 680 685

gga agg gat gtg aca agt gtg gaa ccc cca agt gtg agt cca gca cgt 2231
Gly Arg Asp Val Thr Ser Val Glu Pro Pro Ser Val Ser Pro Ala Arg
690 695 700

cac cag ctt aca agt gca ctc agt cgt atg act cag ggg cta cgc tgg 2279
His Gln Leu Thr Ser Ala Leu Ser Arg Met Thr Gln Gly Leu Arg Trp
705 710 715 720

gta cgt ttt aca tta gga cga tca agt tcc cta agt cag aac cag agt 2327
Val Arg Phe Thr Leu Gly Arg Ser Ser Ser Leu Ser Gln Asn Gln Ser
725 730 735

cct ttg aga caa ctt gat aat ggg gta agt gga aga gaa gat gat gat 2375
Pro Leu Arg Gln Leu Asp Asn Gly Val Ser Gly Arg Glu Asp Asp Asp
740 745 750

gat gtt gaa atg cta att cca att tct gat gga tct tca gac ttt gat 2423
Asp Val Glu Met Leu Ile Pro Ile Ser Asp Gly Ser Ser Asp Phe Asp
755 760 765

gtg aat gac tgc tcc aga cct ctt ctt gat ctt gcc tca gat caa gga 2471
Val Asn Asp Cys Ser Arg Pro Leu Leu Asp Leu Ala Ser Asp Gln Gly
770 775 780

caa ggg ctt aga caa cca tat aat gca aca aat cct gga gta agg cca 2519
Gln Gly Leu Arg Gln Pro Tyr Asn Ala Thr Asn Pro Gly Val Arg Pro
785 790 795 800

agt aat cga gat ggc ccc tgt gag cgc tgt ggt att gtc cac act gcc 2567
Ser Asn Arg Asp Gly Pro Cys Glu Arg Cys Gly Ile Val His Thr Ala
805 810 815

cag ata cca gac act tgc tta gaa gta aca ctg aaa aac gaa acg agt 2615
Gln Ile Pro Asp Thr Cys Leu Glu Val Thr Leu Lys Asn Glu Thr Ser
820 825 830

gat gat gag gct ttg tta ctt tgt taggtacgaa tcacataagg gagattgtat 2669
Asp Asp Glu Ala Leu Leu Cys
835 840

acaagttgga gcaatatcca ttattattt tgtaacttta cagttaaact agttttagtt 2729

taaaaagaaa aaatgcaggg tgatttcta ttattatag ttagcctgca tggtaaatt 2789

cgacaacttg taactctatg aacttagagt ttactatttt agcagctaaa aatgcatcac 2849

atattgcata ttgttcaata atggctcttt catttgtttc tgattgtttt catcctgata 2909

ctgtagttca ctgtagaaat gtggctgctg aaactcattt gattgtcatt ttatctatc 2969

ctatgttaaa tggttgttt ttacaaaata atacctatt ttaattgaaa cgtttatgct 3029

ttgccaagc acatcttgta acttaataata gctagatggt aagggtgta atgtaccaa 3089

aaaaaaaaac ctatactca cctgcgtttt catttgttg acatttgtct attattggat 3149

atcattatca tatgaacttg tcagtgggaa acaactgtc taaaaattta tctcttacgt 3209

ttaacatata atcatgtgag atttaggcag agttcgataa attactggca aaaacaaaac 3269

tcattataa agattttcta atgttgactt taatactcta acatgtgata aaccanatgg 3329

taaaatc

3336

<210> 28
<211> 840
<212> PRT
<213> Homo sapiens
<223> n 3325 can be A, G, C, or T.

<400> 28
Met Ala Cys Arg Trp Ser Thr Lys Glu Ser Pro Arg Trp Arg Ser Ala
1 5 10 15
Leu Leu Leu Leu Phe Leu Ala Gly Val Tyr Ala Cys Gly Glu Thr Pro
20 25 30
Glu Gln Ile Arg Ala Pro Ser Gly Ile Ile Thr Ser Pro Gly Trp Pro
35 40 45
Ser Glu Tyr Pro Ala Lys Ile Asn Cys Ser Trp Phe Ile Arg Ala Asn
50 55 60
Pro Gly Glu Ile Ile Thr Ile Ser Phe Gln Asp Phe Asp Ile Gln Gly
65 70 75 80
Ser Arg Arg Cys Asn Leu Asp Trp Leu Thr Ile Glu Thr Tyr Lys Asn
85 90 95
Ile Glu Ser Tyr Arg Ala Cys Gly Ser Thr Ile Pro Pro Pro Tyr Ile
100 105 110
Ser Ser Gln Asp His Ile Trp Ile Arg Phe His Ser Asp Asp Asn Ile
115 120 125
Ser Arg Lys Gly Phe Arg Leu Ala Tyr Phe Ser Gly Lys Ser Glu Glu
130 135 140
Pro Asn Cys Ala Cys Asp Gln Phe Arg Cys Gly Asn Gly Lys Cys Ile
145 150 155 160
Pro Glu Ala Trp Lys Cys Asn Asn Met Asp Glu Cys Gly Asp Ser Ser
165 170 175
Asp Glu Glu Ile Cys Ala Lys Glu Ala Asn Pro Pro Thr Ala Ala Ala
180 185 190
Phe Gln Pro Cys Ala Tyr Asn Gln Phe Gln Cys Leu Ser Arg Phe Thr
195 200 205
Lys Val Tyr Thr Cys Leu Pro Glu Ser Leu Lys Cys Asp Gly Asn Ile
210 215 220
Asp Cys Leu Asp Leu Gly Asp Glu Ile Asp Cys Asp Val Pro Thr Cys
225 230 235 240
Gly Gln Trp Leu Lys Tyr Phe Tyr Gly Thr Phe Asn Ser Pro Asn Tyr

245	250	255
Pro Asp Phe Tyr Pro Pro Gly Ser Asn Cys Thr Trp Leu Ile Asp Thr		
260	265	270
Gly Asp His Arg Lys Val Ile Leu Arg Phe Thr Asp Phe Lys Leu Asp		
275	280	285
Gly Thr Gly Tyr Gly Asp Tyr Val Lys Ile Tyr Asp Gly Leu Glu Glu		
290	295	300
Asn Pro His Lys Leu Leu Arg Val Leu Thr Ala Phe Asp Ser His Ala		
305	310	315
Pro Leu Thr Val Val Ser Ser Ser Gly Gln Ile Arg Val His Phe Cys		
325	330	335
Ala Asp Lys Val Asn Ala Ala Arg Gly Phe Asn Ala Thr Tyr Gln Val		
340	345	350
Asp Gly Phe Cys Leu Pro Trp Glu Ile Pro Cys Gly Gly Asn Trp Gly		
355	360	365
Cys Tyr Thr Glu Gln Gln Arg Cys Asp Gly Tyr Trp His Cys Pro Asn		
370	375	380
Gly Arg Asp Glu Thr Asn Cys Thr Met Cys Gln Lys Glu Glu Phe Pro		
385	390	395
Cys Ser Arg Asn Gly Val Cys Tyr Pro Arg Ser Asp Arg Cys Asn Tyr		
405	410	415
Gln Asn His Cys Pro Asn Gly Ser Asp Glu Lys Asn Cys Phe Phe Cys		
420	425	430
Gln Pro Gly Asn Phe His Cys Lys Asn Asn Arg Cys Val Phe Glu Ser		
435	440	445
Trp Val Cys Asp Ser Gln Asp Asp Cys Gly Asp Gly Ser Asp Glu Glu		
450	455	460
Asn Cys Pro Val Ile Val Pro Thr Arg Val Ile Thr Ala Ala Val Ile		
465	470	475
Gly Ser Leu Ile Cys Gly Leu Leu Leu Val Ile Ala Leu Gly Cys Thr		
485	490	495
Cys Lys Leu Tyr Ser Leu Arg Met Phe Glu Arg Arg Ser Phe Glu Thr		
500	505	510
Gln Leu Ser Arg Val Glu Ala Glu Leu Leu Arg Arg Glu Ala Pro Pro		
515	520	525

Ser Tyr Gly Gln Leu Ile Ala Gln Gly Leu Ile Pro Pro Val Glu Asp
530 535 540

Phe Pro Val Cys Ser Pro Asn Gln Ala Ser Val Leu Glu Asn Leu Arg
545 550 555 560

Leu Ala Val Arg Ser Gln Leu Gly Phe Thr Ser Val Arg Leu Pro Met
565 570 575

Ala Gly Arg Ser Ser Asn Ile Trp Asn Arg Ile Phe Asn Phe Ala Arg
580 585 590

Ser Arg His Ser Gly Ser Leu Ala Leu Val Ser Ala Asp Gly Asp Glu
595 600 605

Val Val Pro Ser Gln Ser Thr Ser Arg Glu Pro Glu Arg Asn His Thr
610 615 620

His Arg Ser Leu Phe Ser Val Glu Ser Asp Asp Thr Asp Thr Glu Asn
625 630 635 640

Glu Arg Arg Asp Met Ala Gly Ala Ser Gly Gly Val Ala Ala Pro Leu
645 650 655

Pro Gln Lys Val Pro Pro Thr Thr Ala Val Glu Ala Thr Val Gly Ala
660 665 670

Cys Ala Ser Ser Ser Thr Gln Ser Thr Arg Gly Gly His Ala Asp Asn
675 680 685

Gly Arg Asp Val Thr Ser Val Glu Pro Pro Ser Val Ser Pro Ala Arg
690 695 700

His Gln Leu Thr Ser Ala Leu Ser Arg Met Thr Gln Gly Leu Arg Trp
705 710 715 720

Val Arg Phe Thr Leu Gly Arg Ser Ser Ser Leu Ser Gln Asn Gln Ser
725 730 735

Pro Leu Arg Gln Leu Asp Asn Gly Val Ser Gly Arg Glu Asp Asp Asp
740 745 750

Asp Val Glu Met Leu Ile Pro Ile Ser Asp Gly Ser Ser Asp Phe Asp
755 760 765

Val Asn Asp Cys Ser Arg Pro Leu Leu Asp Leu Ala Ser Asp Gln Gly
770 775 780

Gln Gly Leu Arg Gln Pro Tyr Asn Ala Thr Asn Pro Gly Val Arg Pro
785 790 795 800

Ser Asn Arg Asp Gly Pro Cys Glu Arg Cys Gly Ile Val His Thr Ala
805 810 815

Gln Ile Pro Asp Thr Cys Leu Glu Val Thr Leu Lys Asn Glu Thr Ser
820 825 830

Asp Asp Glu Ala Leu Leu Leu Cys
835 840

<210> 29

<211> 1498

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (120)..(1466)

<400> 29

cgccggtggc tcggcggcgg cggcggcggc ggccgcggcg gcggcggcgg cgtcgtctac 60

ctccagctcc tctcctcc tctcgtct cctcctct ctcctatct gctgtggtt 119

atg gcc tgt cgc tgg agc aca aaa gag tct ccg cgg tgg agg tct gcg 167

Met Ala Cys Arg Trp Ser Thr Lys Glu Ser Pro Arg Trp Arg Ser Ala

1 5 10 15

ttg ctc ttg ctt ttc ctc gct ggg gtg tac gga aat ggt gct ctt gca 215

Leu Leu Leu Leu Phe Leu Ala Gly Val Tyr Gly Asn Gly Ala Leu Ala

20 25 30

gaa cat tct gaa aat gtg cat att tca gga gtg tca act gct tgt gga 263

Glu His Ser Glu Asn Val His Ile Ser Gly Val Ser Thr Ala Cys Gly

35 40 45

gag act cca gag caa ata cga gca cca agt ggc ata atc aca agc cca 311

Glu Thr Pro Glu Gln Ile Arg Ala Pro Ser Gly Ile Ile Thr Ser Pro

50 55 60

ggc tgg cct tct gaa tat cct gca aaa atc aac tgt agc tgg ttc ata 359

Gly Trp Pro Ser Glu Tyr Pro Ala Lys Ile Asn Cys Ser Trp Phe Ile

65 70 75 80

agg gca aac cca ggc gaa atc att act ata agt ttt cag gat ttt gat 407

Arg Ala Asn Pro Gly Glu Ile Ile Thr Ile Ser Phe Gln Asp Phe Asp

85 90 95

att caa gga tcc aga agg tgc aat ttg gac tgg ttg aca ata gaa aca 455

Ile Gln Gly Ser Arg Arg Cys Asn Leu Asp Trp Leu Thr Ile Glu Thr

100 105 110

tac aag aat att gaa agt tac aga gct tgt ggt tcc aca att cca cct 503

Tyr Lys Asn Ile Glu Ser Tyr Arg Ala Cys Gly Ser Thr Ile Pro Pro

115	120	125	
ccg tat atc tct tca caa gac cac atc tgg att agg ttt cat tcg gat 551			
Pro Tyr Ile Ser Ser Gln Asp His Ile Trp Ile Arg Phe His Ser Asp			
130	135	140	
gac aac atc tct aga aag ggt ttc aga ctg gca tat ttt tca ggg aaa 599			
Asp Asn Ile Ser Arg Lys Gly Phe Arg Leu Ala Tyr Phe Ser Gly Lys			
145	150	155	160
tct gag gaa cca aat tgt gct tgt gat cag ttt cgt tgt ggt aat gga 647			
Ser Glu Glu Pro Asn Cys Ala Cys Asp Gln Phe Arg Cys Gly Asn Gly			
165	170	175	
aag tgt ata cca gaa gcc tgg aaa tgt aat aac atg gat gaa tgt gga 695			
Lys Cys Ile Pro Glu Ala Trp Lys Cys Asn Asn Met Asp Glu Cys Gly			
180	185	190	
gat agt tcc gat gaa gag atc tgt gcc aaa gaa gca aat cct cca act 743			
Asp Ser Ser Asp Glu Glu Ile Cys Ala Lys Glu Ala Asn Pro Pro Thr			
195	200	205	
gct gct gct ttt caa ccc tgt gct tac aac cag ttc cag tgt tta tcc 791			
Ala Ala Ala Phe Gln Pro Cys Ala Tyr Asn Gln Phe Gln Cys Leu Ser			
210	215	220	
cgt ttt acc aaa gtt tac act tgc ctc ccc gaa tct tta aaa tgt gat 839			
Arg Phe Thr Lys Val Tyr Thr Cys Leu Pro Glu Ser Leu Lys Cys Asp			
225	230	235	240
ggg aac att gac tgc ctt gac cta gga gat gag ata gac tgt gat gtg 887			
Gly Asn Ile Asp Cys Leu Asp Leu Gly Asp Glu Ile Asp Cys Asp Val			
245	250	255	
cca aca tgt ggg caa tgg cta aaa tat ttt tat ggt act ttt aat tct 935			
Pro Thr Cys Gly Gln Trp Leu Lys Tyr Phe Tyr Gly Thr Phe Asn Ser			
260	265	270	
ccc aat tat cca gac ttt tat cct cct gga agc aat tgc acc tgg tta 983			
Pro Asn Tyr Pro Asp Phe Tyr Pro Pro Gly Ser Asn Cys Thr Trp Leu			
275	280	285	
ata gac act ggt gat cac cgt aaa gtc att tta cgc ttc act gac ttt 1031			
Ile Asp Thr Gly Asp His Arg Lys Val Ile Leu Arg Phe Thr Asp Phe			
290	295	300	
aaa ctt gat ggt act ggt tat ggt gat tat gtc aaa ata tat gat gga 1079			
Lys Leu Asp Gly Thr Gly Tyr Asp Tyr Val Lys Ile Tyr Asp Gly			
305	310	315	320
tta gag gag aat cca cac aag ctt ttg cgt gtg ttg aca gct ttt gat 1127			
Leu Glu Glu Asn Pro His Lys Leu Leu Arg Val Leu Thr Ala Phe Asp			
325	330	335	

tct cat gca cct ctt aca gtt gtt tct tct tct gga cag ata agg gta 1175
 Ser His Ala Pro Leu Thr Val Val Ser Ser Ser Gly Gln Ile Arg Val
 340 345 350

cat ttt tgt gct gat aaa gtg aat gct gca agg gga ttt aat gct act 1223
 His Phe Cys Ala Asp Lys Val Asn Ala Ala Arg Gly Phe Asn Ala Thr
 355 360 365

tac caa gta gat ggg ttc tgt ttg cca tgg gaa ata ccc tgt gga ggt 1271
 Tyr Gln Val Asp Gly Phe Cys Leu Pro Trp Glu Ile Pro Cys Gly Gly
 370 375 380

aac tgg ggg tgt tat act gag cag cag cgt cgt gat ggg tat tgg cat 1319
 Asn Trp Gly Cys Tyr Thr Glu Gln Gln Arg Arg Asp Gly Tyr Trp His
 385 390 395 400

tgc cca aat gga agg gat gaa acc aat tgt acc atg tgc cag aag gaa 1367
 Cys Pro Asn Gly Arg Asp Glu Thr Asn Cys Thr Met Cys Gln Lys Glu
 405 410 415

gaa ttt cca tgt tcc cga aat ggt gtc tgt tat cct cgt tct gat cgc 1415
 Glu Phe Pro Cys Ser Arg Asn Gly Val Cys Tyr Pro Arg Ser Asp Arg
 420 425 430

tgc aac tac cag aat cat tgc cca aat ggc aaa cag aac cca tct act 1463
 Cys Asn Tyr Gln Asn His Cys Pro Asn Gly Lys Gln Asn Pro Ser Thr
 435 440 445

tgg taagtagcat taaatcccct tgcagcattc ac 1498
 Trp

<210> 30
 <211> 449
 <212> PRT
 <213> Homo sapiens

<400> 30
 Met Ala Cys Arg Trp Ser Thr Lys Glu Ser Pro Arg Trp Arg Ser Ala
 1 5 10 15

Leu Leu Leu Leu Phe Leu Ala Gly Val Tyr Gly Asn Gly Ala Leu Ala
 20 25 30

Glu His Ser Glu Asn Val His Ile Ser Gly Val Ser Thr Ala Cys Gly
 35 40 45

Glu Thr Pro Glu Gln Ile Arg Ala Pro Ser Gly Ile Ile Thr Ser Pro
 50 55 60

Gly Trp Pro Ser Glu Tyr Pro Ala Lys Ile Asn Cys Ser Trp Phe Ile
 65 70 75 80

Arg Ala Asn Pro Gly Glu Ile Ile Thr Ile Ser Phe Gln Asp Phe Asp
85 90 95

Ile Gln Gly Ser Arg Arg Cys Asn Leu Asp Trp Leu Thr Ile Glu Thr
100 105 110

Tyr Lys Asn Ile Glu Ser Tyr Arg Ala Cys Gly Ser Thr Ile Pro Pro
115 120 125

Pro Tyr Ile Ser Ser Gln Asp His Ile Trp Ile Arg Phe His Ser Asp
130 135 140

Asp Asn Ile Ser Arg Lys Gly Phe Arg Leu Ala Tyr Phe Ser Gly Lys
145 150 155 160

Ser Glu Glu Pro Asn Cys Ala Cys Asp Gln Phe Arg Cys Gly Asn Gly
165 170 175

Lys Cys Ile Pro Glu Ala Trp Lys Cys Asn Asn Met Asp Glu Cys Gly
180 185 190

Asp Ser Ser Asp Glu Glu Ile Cys Ala Lys Glu Ala Asn Pro Pro Thr
195 200 205

Ala Ala Ala Phe Gln Pro Cys Ala Tyr Asn Gln Phe Gln Cys Leu Ser
210 215 220

Arg Phe Thr Lys Val Tyr Thr Cys Leu Pro Glu Ser Leu Lys Cys Asp
225 230 235 240

Gly Asn Ile Asp Cys Leu Asp Leu Gly Asp Glu Ile Asp Cys Asp Val
245 250 255

Pro Thr Cys Gly Gln Trp Leu Lys Tyr Phe Tyr Gly Thr Phe Asn Ser
260 265 270

Pro Asn Tyr Pro Asp Phe Tyr Pro Pro Gly Ser Asn Cys Thr Trp Leu
275 280 285

Ile Asp Thr Gly Asp His Arg Lys Val Ile Leu Arg Phe Thr Asp Phe
290 295 300

Lys Leu Asp Gly Thr Gly Tyr Gly Asp Tyr Val Lys Ile Tyr Asp Gly
305 310 315 320

Leu Glu Glu Asn Pro His Lys Leu Leu Arg Val Leu Thr Ala Phe Asp
325 330 335

Ser His Ala Pro Leu Thr Val Val Ser Ser Ser Gly Gln Ile Arg Val
340 345 350

His Phe Cys Ala Asp Lys Val Asn Ala Ala Arg Gly Phe Asn Ala Thr

355	360	365
Tyr Gln Val Asp Gly Phe Cys Leu Pro Trp Glu Ile Pro Cys Gly Gly		
370	375	380
Asn Trp Gly Cys Tyr Thr Glu Gln Gln Arg Arg Asp Gly Tyr Trp His		
385	390	400
Cys Pro Asn Gly Arg Asp Glu Thr Asn Cys Thr Met Cys Gln Lys Glu		
405	410	415
Glu Phe Pro Cys Ser Arg Asn Gly Val Cys Tyr Pro Arg Ser Asp Arg		
420	425	430
Cys Asn Tyr Gln Asn His Cys Pro Asn Gly Lys Gln Asn Pro Ser Thr		
435	440	445

Trp

<210> 31
 <211> 691
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (203)..(571)

<400> 31
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 ctccgggagc ggcagcagta gcccgggcgg cgagggtgg gggttcctcg agactctcag 120
 aggggcgcct cccatcggcg cccaccaccc caactgttc ctgcgcgcc actgcgctgc 180
 gccccaggac ccgctgccca ac atg gat ttt ctc ctg gcg ctg gtg ctg gta 232
 Met Asp Phe Leu Leu Ala Leu Val Leu Val
 1 5 10
 tcc tcg ctc tac ctg cag gcg gcc gcc gag tac gac ggg agg tgg ccc 280
 Ser Ser Leu Tyr Leu Gln Ala Ala Ala Glu Tyr Asp Gly Arg Trp Pro
 15 20 25
 agg caa ata gtg tca tcg att ggc cta tgt cgt tat ggt ggg agg att 328
 Arg Gln Ile Val Ser Ser Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile
 30 35 40
 gac tgc tgc tgg ggc tgg gct cgc cag tct tgg gga cag tgt cag cct 376
 Asp Cys Cys Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro
 45 50 55

ttc tac gtc tta agg cag aga ata gcc agg ata agg tgc cag ctc aaa 424
Phe Tyr Val Leu Arg Gln Arg Ile Ala Arg Ile Arg Cys Gln Leu Lys
60 65 70

gct gtg tgc caa cca cga tgc aaa cat ggt gaa tgt atc ggg cca aac 472
Ala Val Cys Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn
75 80 85 90

aag tgc aag tgt cat cct ggt tat gct gga aaa acc tgt aat caa gcc 520
Lys Cys Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Ala
95 100 105

gta ggt ttt gaa aga tgt atg gtt cca gcc ggg cgc cgt ggc tct acc 568
Val Gly Phe Glu Arg Cys Met Val Pro Ala Gly Arg Arg Gly Ser Thr
110 115 120

ctg taatcccagc actttggaag gccgaggcgg gcggatcacg aggtcaggat 621
Leu

atcgagacca tcctggctaa cacggtgaaa ccccatctct actaaaaata caaaaaaaaa 681

aaaaaaaaaa 691

<210> 32
<211> 123
<212> PRT
<213> Homo sapiens

<400> 32
Met Asp Phe Leu Leu Ala Leu Val Leu Val Ser Ser Leu Tyr Leu Gln
1 5 10 15

Ala Ala Ala Glu Tyr Asp Gly Arg Trp Pro Arg Gln Ile Val Ser Ser
20 25 30

Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys Trp Gly Trp
35 40 45

Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Phe Tyr Val Leu Arg Gln
50 55 60

Arg Ile Ala Arg Ile Arg Cys Gln Leu Lys Ala Val Cys Gln Pro Arg
65 70 75 80

Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys Lys Cys His Pro
85 90 95

Gly Tyr Ala Gly Lys Thr Cys Asn Gln Ala Val Gly Phe Glu Arg Cys
100 105 110

Met Val Pro Ala Gly Arg Arg Gly Ser Thr Leu

120

<220>
<221> CDS
<222> (203)..(1948)

<400> 33
gggagggggc tccgggcgcc ggcgcgcaga cctgctccgg ccgcgcgcct cgccgctgtc 60

aggggcgctt cccatcggcg cccaccacc caacctgttc ctcgcgcgc actgcgctgc 180

Met Asp Phe Leu Leu Ala Leu Val Leu Val
1 5 10

tcc tcg ctc tac ctg cag gcg gcc gag ttc gac ggg ggg ggg
Ser Ser Leu Tyr Leu Gln Ala Ala Ala Glu Phe Asp Gly Arg Trp Pro
15 20 25

agg caa ata gtg tca ttc att ggc caa tgc cgc tat ggt ggg ggg
Arg Gln Ile Val Ser Ser Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile
30 35 40

gac tgc tgc tgg ggc tgg gct tgc cag tct tgg gga cag tgc tgc tgc
Asp Cys Cys Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro
45 50 55

Phe Tyr Val Leu Arg Gln Arg Ile Ala Arg Ile Arg Cys Gln Leu Lys
60 65 70

gct gtg tgc caa cca cga tgc aaa cat ggc gaa tgc cca ggc
Ala Val Cys Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn
75 80 85 90

Lys Cys Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Ile Gln Val
95 100 105

Leu Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met.

aac act tac ggc agc tac aag tgc tac tgt ctc aac gga tat atg ctc 616

Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met Leu
125 130 135

atg ccg gat ggt tcc tgc tca agt gcc ctg acc tgc tcc atg gca aac 664
Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met Ala Asn
140 145 150

tgt cag tat ggc tgt gat gtt gtt aaa gga caa ata cgg tgc cag tgc 712
Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg Cys Gln Cys
155 160 165 170

cca tcc cct ggc ctg cag ctg gct cct gat ggg agg acc tgt gta gat 760
Pro Ser Pro Gly Leu Gln Leu Ala Pro Asp Gly Arg Thr Cys Val Asp
175 180 185

gtt gat gaa tgt gct aca gga aga gcc tcc tgc cct aga ttt agg caa 808
Val Asp Glu Cys Ala Thr Gly Arg Ala Ser Cys Pro Arg Phe Arg Gln
190 195 200

tgt gtc aac act ttt ggg agc tac atc tgc aag tgt cat aaa ggc ttc 856
Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys Lys Cys His Lys Gly Phe
205 210 215

gat ctc atg tat att gga ggc aaa tat caa tgt cat gac ata gac gaa 904
Asp Leu Met Tyr Ile Gly Lys Tyr Gln Cys His Asp Ile Asp Glu
220 225 230

tgc tca ctt ggt cag tat cag tgc agc agc ttt gct cga tgt tat aac 952
Cys Ser Leu Gly Gln Tyr Gln Cys Ser Ser Phe Ala Arg Cys Tyr Asn
235 240 245 250

gta cgt ggg tcc tac aag tgc aaa tgt aaa gaa gga tac cag ggt gat 1000
Val Arg Gly Ser Tyr Lys Cys Lys Cys Lys Glu Gly Tyr Gln Gly Asp
255 260 265

gga ctg act tgt gtg tat atc cca aaa gtt atg att gaa cct tca ggt 1048
Gly Leu Thr Cys Val Tyr Ile Pro Lys Val Met Ile Glu Pro Ser Gly
270 275 280

cca att cat gta cca aag gga aat ggt acc att tta aag ggt gac aca 1096
Pro Ile His Val Pro Lys Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr
285 290 295

gga aat aat aat tgg att cct gat gtt gga agt act tgg tgg cct ccg 1144
Gly Asn Asn Asn Trp Ile Pro Asp Val Gly Ser Thr Trp Trp Pro Pro
300 305 310

aag aca cca tat att cct cct atc att acc aac agg cct act tct aag 1192
Lys Thr Pro Tyr Ile Pro Pro Ile Ile Thr Asn Arg Pro Thr Ser Lys
315 320 325 330

cca aca aca aga cct aca cca aag cca aca cca att cct act cca cca 1240
Pro Thr Thr Arg Pro Thr Pro Lys Pro Thr Pro Ile Pro Thr Pro Pro

335

340

345

cca cca cca ccc ctg cca aca gag ctc aga aca cct cta cca cct aca 1288
 Pro Pro Pro Pro Leu Pro Thr Glu Leu Arg Thr Pro Leu Pro Pro Thr
 350 355 360

acc cca gaa agg cca acc acc gga ctg aca act ata gca cca gct gcc 1336
 Thr Pro Glu Arg Pro Thr Thr Gly Leu Thr Thr Ile Ala Pro Ala Ala
 365 370 375

agt aca cct cca gga ggg att aca gtt gac aac agg gta cag aca gac 1384
 Ser Thr Pro Pro Gly Gly Ile Thr Val Asp Asn Arg Val Gln Thr Asp
 380 385 390

cct cag aaa ccc aga gga gat gtg ttc att cca cgg caa cct tca aat 1432
 Pro Gln Lys Pro Arg Gly Asp Val Phe Ile Pro Arg Gln Pro Ser Asn
 395 400 405 410

gac ttg ttt gaa ata ttt gaa ata gaa aga gga gtc agt gca gac gat 1480
 Asp Leu Phe Glu Ile Phe Glu Ile Glu Arg Gly Val Ser Ala Asp Asp
 415 420 425

gaa gca aag gat gat cca ggt gtt ctg gta cac agt tgt aat ttt gac 1528
 Glu Ala Lys Asp Asp Pro Gly Val Leu Val His Ser Cys Asn Phe Asp
 430 435 440

cat gga ctt tgt gga tgg atc agg gag aaa gac aat gac ttg cac tgg 1576
 His Gly Leu Cys Gly Trp Ile Arg Glu Lys Asp Asn Asp Leu His Trp
 445 450 455

gaa cca atc agg gac cca gca ggt gga caa tat ctg aca gtg tgg gca 1624
 Glu Pro Ile Arg Asp Pro Ala Gly Gly Gln Tyr Leu Thr Val Ser Ala
 460 465 470

gcc aaa gcc cca ggg gga aaa gct gca cgc ttg gtg cta cct ctc ggc 1672
 Ala Lys Ala Pro Gly Gly Lys Ala Ala Arg Leu Val Leu Pro Leu Gly
 475 480 485 490

cgc ctt atg cat tca ggg gac ctg tgc ctg tca ttc agg cac aag gtg 1720
 Arg Leu Met His Ser Gly Asp Leu Cys Leu Ser Phe Arg His Lys Val
 495 500 505

acg ggg ctg cac tct ggc aca ctc cag gtg ttt gtg aga aaa cac ggt 1768
 Thr Gly Leu His Ser Gly Thr Leu Gln Val Phe Val Arg Lys His Gly
 510 515 520

gcc cac gga gca gcc ctg tgg gga aga aat ggt ggc cat ggc tgg agg 1816
 Ala His Gly Ala Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg
 525 530 535

caa aca cag atc acc ttg cga ggg gct gac atc aag agc gtc gtc ttc 1864
 Gln Thr Gln Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Val Val Phe
 540 545 550

aaa ggt gaa aaa agg cgt ggt cac act ggg gag att gga tta gat gat 1912
Lys Gly Glu Lys Arg Arg Gly His Thr Gly Glu Ile Gly Leu Asp Asp
555 560 565 570

gtg agc ttg aaa aaa ggc cac tgc tct gaa gaa cgc taacaactcc 1958
Val Ser Leu Lys Lys Gly His Cys Ser Glu Glu Arg
575 580

agaactaaca atgaactcct atgttgctct atcctctttt tccaattctc atcttctctc 2018

ctcttctccc ttttatcagg cctaggagaa gagtgggtca gtgggtcaga aggaagtcta 2078

tttggtgacc caggttcttc tggcctgctt ttgt 2112

<210> 34

<211> 582

<212> PRT

<213> Homo sapiens

<400> 34

Met Asp Phe Leu Leu Ala Leu Val Leu Val Ser Ser Leu Tyr Leu Gln
1 5 10 15

Ala Ala Ala Glu Phe Asp Gly Arg Trp Pro Arg Gln Ile Val Ser Ser
20 25 30

Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys Trp Gly Trp
35 40 45

Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Phe Tyr Val Leu Arg Gln
50 55 60

Arg Ile Ala Arg Ile Arg Cys Gln Leu Lys Ala Val Cys Gln Pro Arg
65 70 75 80

Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys Lys Cys His Pro
85 90 95

Gly Tyr Ala Gly Lys Thr Cys Ile Gln Val Leu Asn Glu Cys Gly Leu
100 105 110

Lys Pro Arg Pro Cys Lys His Arg Cys Met Asn Thr Tyr Gly Ser Tyr
115 120 125

Lys Cys Tyr Cys Leu Asn Gly Tyr Met Leu Met Pro Asp Gly Ser Cys
130 135 140

Ser Ser Ala Leu Thr Cys Ser Met Ala Asn Cys Gln Tyr Gly Cys Asp
145 150 155 160

Val Val Lys Gly Gln Ile Arg Cys Gln Cys Pro Ser Pro Gly Leu Gln

165	170	175
Leu Ala Pro Asp Gly Arg Thr Cys Val Asp Val Asp Glu Cys Ala Thr		
180	185	190
Gly Arg Ala Ser Cys Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly		
195	200	205
Ser Tyr Ile Cys Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly		
210	215	220
Gly Lys Tyr Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr		
225	230	235
Gln Cys Ser Ser Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys		
245	250	255
Cys Lys Cys Lys Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr		
260	265	270
Ile Pro Lys Val Met Ile Glu Pro Ser Gly Pro Ile His Val Pro Lys		
275	280	285
Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn Trp Ile		
290	295	300
Pro Asp Val Gly Ser Thr Trp Trp Pro Pro Lys Thr Pro Tyr Ile Pro		
305	310	315
Pro Ile Ile Thr Asn Arg Pro Thr Ser Lys Pro Thr Thr Arg Pro Thr		
325	330	335
Pro Lys Pro Thr Pro Ile Pro Thr Pro Pro Pro Pro Pro Leu Pro		
340	345	350
Thr Glu Leu Arg Thr Pro Leu Pro Pro Thr Thr Pro Glu Arg Pro Thr		
355	360	365
Thr Gly Leu Thr Thr Ile Ala Pro Ala Ala Ser Thr Pro Pro Gly Gly		
370	375	380
Ile Thr Val Asp Asn Arg Val Gln Thr Asp Pro Gln Lys Pro Arg Gly		
385	390	395
Asp Val Phe Ile Pro Arg Gln Pro Ser Asn Asp Leu Phe Glu Ile Phe		
405	410	415
Glu Ile Glu Arg Gly Val Ser Ala Asp Asp Glu Ala Lys Asp Asp Pro		
420	425	430
Gly Val Leu Val His Ser Cys Asn Phe Asp His Gly Leu Cys Gly Trp		
435	440	445

Ile Arg Glu Lys Asp Asn Asp Leu His Trp Glu Pro Ile Arg Asp Pro
450 455 460

Ala Gly Gly Gln Tyr Leu Thr Val Ser Ala Ala Lys Ala Pro Gly Gly
465 470 475 480

Lys Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly
485 490 495

Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser Gly
500 505 510

Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala Ala Leu
515 520 525

Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln Ile Thr Leu
530 535 540

Arg Gly Ala Asp Ile Lys Ser Val Val Phe Lys Gly Glu Lys Arg Arg
545 550 555 560

Gly His Thr Gly Glu Ile Gly Leu Asp Asp Val Ser Leu Lys Lys Gly
565 570 575

His Cys Ser Glu Glu Arg
580

<210> 35

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 35

gaattcttgc caagagagta cacagtcatt aatg

34

<210> 36

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 36

aagcttttgc caagagagta cacagtcatt aatg

34

<210> 37
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 37
ctcgagtttc atatttcttt caatccagtc 30

<210> 38
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 38
tgtggccagg ttctgcga 18

<210> 39
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 39
cttgacaagg ctggatct 18

<210> 40
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 40
cctaccaaga agccagcc 18

<210> 41
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 41

tcgcagaacc tggccaca

18

<210> 42

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 42

agatccagcc ttgtcaag

18

<210> 43

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 43

ggctggcttc ttgtagg

18

<210> 44

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 44

caggcagcca tctacaggag g

21

<210> 45

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 45

cctcctgtag atggctgcct g

21

<210> 46
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 46
caggagtccc acatcact 18

<210> 47
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 47
agtgatgtgg gactcctg 18

<210> 48
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 48
gctagccacc atggagctgg gttgctggac gcagttgg 38

<210> 49
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 49
aggacgtgga gtgaggatcc tatgctctgg atagg 35

<210> 50
<211> 30
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 50

ctcgtcctcg agggtaagcc tatccctaac 30

<210> 51

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 51

ctcgtcgggc ccctgatcag cggtttaa c 31

<210> 52

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 52

ggatccaaat cctgtccatc tgtgtgtcgc tg 32

<210> 53

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 53

ctcgagagcc aaaggtaa tggggtttt gtaag 35

<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 54
cgagacagca actatctc 18

<210> 55
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 55
cgactggata tgtccaat 18

<210> 56
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 56
acaattactg tgaagtct 18

<210> 57
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 57
gagatagttg ctgtctcg 18

<210> 58
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 58
attggacata tccagtcg 18

<210> 59

<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 59
agacttcaca gtaattgt 18

<210> 60
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 60
ggatccgagg ctgaaggcaa tgcaagctgc acag 34

<210> 61
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 61
tcgagcagtg gaatgtaggt gctgtgaatg cag 33

<210> 62
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 62
ggatccgcgg tcctgtggaa gcatgtgcgg ctg 33

<210> 63
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 63

ctcgagcgtg ttgcacacca gcacatctgc

30

<210> 64

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 64

gacgtggccc tcatcgcaa c

21

<210> 65

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 65

ctaggcgagg agtacattct g

21

<210> 66

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 66

ctggaccggg ctgagcaa

18

<210> 67

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 67

gttggcgatg agggccacgt c

21

<210> 68
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 68
cagaatgtac tcctcgcta g 21

<210> 69
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 69
ttgctcagcc cggccag 18

<210> 70
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 70
ggtacctgtg gagagactcc agagcaaata cga 33

<210> 71
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 71
ctcgagagtg atgactcttg taggcacgat tac 33

<210> 72
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 72
gcttgatgac agtttcgt 18

<210> 73
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 73
tgcacctggt taatagac 18

<210> 74
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 74
actgagcagc agcgttgt 18

<210> 75
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 75
acgaaactga tcacaagc 18

<210> 76
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 76

tattaaccag gtgcaatt 18

<210> 77

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 77

acaacgctgc tgctcagt 18

<210> 78

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 78

ggatccgagt acgacgggag gtggcccagg 30

<210> 79

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 79

ctcgagcagg gtagagccac ggcgcccggc tggaac 36

<210> 80

<211> 261

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: AMPLIFICATION
PRODUCT 16467945.0.85-S259.A

<400> 80

gagtacgacg ggaggtggcc caggcaaata gtgtcatcga ttggcctatg tcgttatggt 60
gggaggattg actgctgctg gggctgggct cgccagtctt ggggacagtg tcagcctgtg 120
tgccaaccac gatgcaaaca tggatgaatg atcgggcca acaagtgcaa gtgtcatcct 180
ggttatgctg gaaaaacctg taatcaagcc gtaggttttg aaagatgtat ggttcagcc 240

<210> 81

<211> 1638

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CONSTRUCT

16467945.0.88-S261.D NUCLEIC ACID

<400> 81

gagttcgacg ggaggtggcc caggcaaata gtgtcatcga ttggcctatg tcgttatggt 60
gggaggattg actgctgctg gggctgggct cgccagtctt ggggacagtg tcagcctgtg 120
tgccaaccac gatgcaaaca tgggtaatgt atcggggcaa acaagtgcaa gtgtcatcct 180
ggttatgctg gaaaaacctg tattcaagtt ttaaatgagt gtggcctgaa gccccggccc 240
tgtaagcaca ggtgcatgaa cacttacggc agctacaagt gctactgtct caacggatat 300
atgctcatgc cggatggttc ctgtcaagt gccctgacct gctccatggc aaactgtcag 360
tatggctgtg atgttgtaa aggacaaata cggtgccagt gcccacccc tggcctgcag 420
ctggctctg atgggaggac ctgtgtagat gttgatgaat gtgtacagg aagagcctcc 480
tgccctagat ttaggcaatg tgtcaacact ttgggagct acatctgcaa gtgtcataaa 540
ggcttcgac tcattgtat tggaggcaaa tatcaatgtc atgacataga cgaatgtca 600
cttggtcagt atcagtgcag cagcttgct cgatgttata acgtacgtgg gtcctacaag 660
tgcaaatgta aagaaggata ccagggtgat ggactgactt gtgtgtatat cccaaaagtt 720
atgattgaac ctcagggtcc aattcatgta ccaaaggga atggtacat ttaaagggt 780
gacacaggaa ataataattg gattcctgat gttggaagta cttggtggcc tccgaagaca 840
ccatatattc ctctatcat taccaacagg cctacttcta agccaacaac aagacctaca 900
ccaaagccaa caccaattcc tactccacca ccaccaccac cctgccaac agagctcaga 960
acacctctac cacctacaac ccagaaaagg ccaaccaccg gactgacaac tatagacca 1020
gctgccagta cacctcagg agggattaca gttgacaaca gggtagacag agaccctcag 1080
aaaccagag gagatgtgt cattccacgg caacctcaa atgacttgtt tgaaatattt 1140
gaaatagaaa gaggagtcag tgcagacgat gaagcaaagg atgatccagg tgttctggta 1200
cacagttgta atttgacca tggacttgtt ggatggatca gggagaaaga caatgacttg 1260
cactgggaac caatcaggga cccagcaggt ggacaatc tgacagtgtc ggcagccaaa 1320
gccccagggg gaaaagctgc acgcttggtg ctacctctcg gccgccttat gcattcaggg 1380
gacctgtgcc tgtcattcag gcacaagggt acggggctgc actctggcac actccagggt 1440
tttgtagaa aacacgggtc ccacggagca gccctgtggg gaagaaatgg tggccatggc 1500
tgagggcaaa cacagatcac cttgcgaggg gctgacatca agagcgtcgt cttcaaaggt 1560
gaaaaaaggc gtggtcacac tggggagatt ggattagatg atgtgagctt gaaaaaaggc 1620
cactgctctg aagaacgc 1638

<210> 82

<211> 546

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TRANSLATION

FROM AMPLIFICATION PRODUCT 16467945.0.88-S261.D

<400> 82

Glu Tyr Asp Gly Arg Trp Pro Arg Gln Ile Val Ser Ser Ile Gly Leu
1 5 10 15

Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys Trp Gly Trp Ala Arg Gln
20 25 30

Ser Trp Gly Gln Cys Gln Pro Val Cys Gln Pro Arg Cys Lys His Gly
35 40 45

Glu Cys Ile Gly Pro Asn Lys Cys Lys Cys His Pro Gly Tyr Ala Gly
50 55 60

Lys Thr Cys Ile Gln Val Leu Asn Glu Cys Gly Leu Lys Pro Arg Pro
65 70 75 80

Cys Lys His Arg Cys Met Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys
85 90 95

Leu Asn Gly Tyr Met Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu
100 105 110

Thr Cys Ser Met Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly
115 120 125

Gln Ile Arg Cys Gln Cys Pro Ser Pro Gly Leu Gln Leu Ala Pro Asp
130 135 140

Gly Arg Thr Cys Val Asp Val Asp Glu Cys Ala Thr Gly Arg Ala Ser
145 150 155 160

Cys Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys
165 170 175

Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly Gly Lys Tyr Gln
180 185 190

Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys Ser Ser
195 200 205

Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys Cys Lys Cys Lys
210 215 220

Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr Ile Pro Lys Val
225 230 235 240

Met Ile Glu Pro Ser Gly Pro Ile His Val Pro Lys Gly Asn Gly Thr
245 250 255

Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn Trp Ile Pro Asp Val Gly
260 265 270

Ser Thr Trp Trp Pro Pro Lys Thr Pro Tyr Ile Pro Pro Ile Ile Thr
275 280 285

Asn Arg Pro Thr Ser Lys Pro Thr Thr Arg Pro Thr Pro Lys Pro Thr
290 295 300

Pro Ile Pro Thr Pro Pro Pro Pro Pro Pro Leu Pro Thr Glu Leu Arg
305 310 315 320

Thr Pro Leu Pro Pro Thr Thr Pro Glu Arg Pro Thr Thr Gly Leu Thr
325 330 335

Thr Ile Ala Pro Ala Ala Ser Thr Pro Pro Gly Gly Ile Thr Val Asp
340 345 350

Asn Arg Val Gln Thr Asp Pro Gln Lys Pro Arg Gly Asp Val Phe Ile
355 360 365

Pro Arg Gln Pro Ser Asn Asp Leu Phe Glu Ile Phe Glu Ile Glu Arg
370 375 380

Gly Val Ser Ala Asp Asp Glu Ala Lys Asp Asp Pro Gly Val Leu Val
385 390 395 400

His Ser Cys Asn Phe Asp His Gly Leu Cys Gly Trp Ile Arg Glu Lys
405 410 415

Asp Asn Asp Leu His Trp Glu Pro Ile Arg Asp Pro Ala Gly Gly Gln
420 425 430

Tyr Leu Thr Val Ser Ala Ala Lys Ala Pro Gly Gly Lys Ala Ala Arg
435 440 445

Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly Asp Leu Cys Leu
450 455 460

Ser Phe Arg His Lys Val Thr Gly Leu His Ser Gly Thr Leu Gln Val
465 470 475 480

Phe Val Arg Lys His Gly Ala His Gly Ala Ala Leu Trp Gly Arg Asn
485 490 495

Gly Gly His Gly Trp Arg Gln Thr Gln Ile Thr Leu Arg Gly Ala Asp
500 505 510

Ile Lys Ser Val Val Phe Lys Gly Glu Lys Arg Arg Gly His Thr Gly
515 520 525

Glu Ile Gly Leu Asp Asp Val Ser Leu Lys Lys Gly His Cys Ser Glu
530 535 540

Glu Arg
545

<210> 83
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 83
cagtcaatgg gtaccagaaa ataaca 26

<210> 84
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PROBE

<400> 84
cctgggctta tcaacggacg cca 23

<210> 85
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 85
accacggtgc caatttagc 20

<210> 86
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 86
gctaaatcct gtccatctgt gt 22

<210> 87
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PROBE

<400> 87
tgaaacccgc atcgagcga 20

<210> 88
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 88
atggatgtca gaaagcgtc a 21

<210> 89
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 89
cagtcacaca gctgctctat tctca 25

<210> 90
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PROBE

<400> 90
aaatctaccc cttgcgtggc tggaac 26

<210> 91
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 91
ggacacctcc agggaaacgt 20

<210> 92
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 92
cctgcaaagc cgtgaggt 18

<210> 93
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PROBE

<400> 93
acggcatctc tgtgccgga acc 23

<210> 94
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 94
ggtgtcctgg tagattcgga ag 22

<210> 95
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 95
gtactgccgc cagcttacct 20

<210> 96
<211> 28
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PROBE

<400> 96

cacagagcca gcagtgcac atgacaaa

28

<210> 97

<211> 24

<212> DNA

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24

<210> 98

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<223> Description of Artificial Sequence: PCR PRIMER

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<223> Description of Artificial Sequence: PROBE

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<223> Description of Artificial Sequence: TRANSLATION
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Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys Trp Gly Trp Ala Arg Gln
20 25 30

Ser Trp Gly Gln Cys Gln Pro Val Cys Gln Pro Arg Cys Lys His Gly
35 40 45

Glu Cys Ile Gly Pro Asn Lys Cys Lys Cys His Pro Gly Tyr Ala Gly
50 55 60

Lys Thr Cys Asn Gln Ala Val Gly Phe Glu Arg Cys Met Val Pro Ala
65 70 75 80

Gly Arg Arg Gly Ser Thr Leu
85